GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:01:25 ; Search time 14.8347 Seconds
(without alignments)
1086.923 Million cell updates/sec

Title: US-10-684-957-33
Perfect score: 1119
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1068	95.4	226	4	US-09-456-090A-80	Sequence 80, Appl
2	1068	95.4	226	4	US-09-456-090A-86	Sequence 86, Appl
3	1068	95.4	226	4	US-09-453-234-80	Sequence 80, Appl
4	1068	95.4	226	4	US-09-453-234-86	Sequence 86, Appl
5	1065	95.2	226	4	US-09-456-090A-50	Sequence 50, Appl
6	1065	95.2	226	4	US-09-453-234-50	Sequence 50, Appl
7	1057	94.5	236	4	US-09-859-053-34	Sequence 34, Appl
8	1056	94.4	226	4	US-09-456-090A-74	Sequence 74, Appl
9	1056	94.4	226	4	US-09-453-234-74	Sequence 74, Appl
10	1055.5	94.3	235	4	US-09-472-087-14	Sequence 14, Appl
11	1055.5	94.3	235	4	US-09-472-087-65	Sequence 65, Appl
12	1053	94.1	226	4	US-09-456-090A-42	Sequence 42, Appl
13	1053	94.1	226	4	US-09-453-234-42	Sequence 42, Appl
14	1048	93.7	236	4	US-09-859-053-38	Sequence 38, Appl
15	1045	93.4	224	4	US-09-456-090A-52	Sequence 52, Appl
16	1045	93.4	224	4	US-09-453-234-52	Sequence 52, Appl
17	1044	93.3	226	4	US-09-456-090A-38	Sequence 38, Appl
18	1044	93.3	226	4	US-09-453-234-38	Sequence 38, Appl
19	1043	93.2	226	4	US-09-456-090A-72	Sequence 72, Appl
20	1043	93.2	226	4	US-09-453-234-72	Sequence 72, Appl
21	1039	92.9	224	4	US-09-456-090A-76	Sequence 76, Appl
22	1039	92.9	224	4	US-09-453-234-76	Sequence 76, Appl
23	1039	92.9	234	4	US-09-472-087-17	Sequence 17, Appl
24	1039	92.9	234	4	US-09-472-087-69	Sequence 69, Appl
25	1036	92.6	224	4	US-09-456-090A-44	Sequence 44, Appl
26	1036	92.6	224	4	US-09-456-090A-78	Sequence 78, Appl
27	1036	92.6	224	4	US-09-453-234-44	Sequence 44, Appl
28	1036	92.6	224	4	US-09-453-234-78	Sequence 78, Appl
29	1034	92.4	224	4	US-09-456-090A-40	Sequence 40, Appl
30	1034	92.4	224	4	US-09-453-234-40	Sequence 40, Appl
31	1029.5	92.0	233	4	US-09-472-087-15	Sequence 15, Appl
32	1029.5	92.0	233	4	US-09-472-087-67	Sequence 67, Appl
33	1017	90.9	215	2	US-08-480-753-8	Sequence 8, Appli
34	1003	89.6	236	4	US-09-315-926A-79	Sequence 79, Appl
35	996	89.0	224	4	US-09-456-090A-82	Sequence 82, Appl
36	996	89.0	224	4	US-09-456-090A-88	Sequence 88, Appl
37	996	89.0	224	4	US-09-456-090A-90	Sequence 90, Appl
38	996	89.0	224	4	US-09-453-234-82	Sequence 82, Appl
39	996	89.0	224	4	US-09-453-234-88	Sequence 88, Appl
40	996	89.0	224	4	US-09-453-234-90	Sequence 90, Appl
41	994.5	88.9	235	1	US-08-276-852-153	Sequence 153, App
42	994.5	88.9	235	1	US-08-899-575-153	Sequence 153, App
43	994.5	88.9	235	1	US-08-899-575-153	Sequence 153, App
44	994.5	88.9	235	5	PCT-US95-08743-153	Sequence 153, App
45	994	88.8	224	4	US-09-456-090A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-456-090A-80
; Sequence 80, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-20L
US-09-456-090A-80

Query Match 95.4%; Score 1068; DB 4; Length 226;
Best Local Similarity 95.8%; Pred. No. 1e-76;
Matches 206; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
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Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
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RESULT 2
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars

```
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-33L
US-09-456-090A-86

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
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  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

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Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 3
US-09-453-234-80
; Sequence 80, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-20L
US-09-453-234-80

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 1e-76;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

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RESULT 4
US-09-453-234-86
; Sequence 86, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-33L
US-09-453-234-86

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 1e-76;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

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RESULT 5
US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
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; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match 95.2%; Score 1065; DB 4; Length 226;
Best Local Similarity 95.8%; Pred. No. 1.7e-76;
Matches 206; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
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Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
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RESULT 6
US-09-453-234-50
; Sequence 50, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-453-234-50

Query Match 95.2%; Score 1065; DB 4; Length 226;
Best Local Similarity 95.8%; Pred. No. 1.7e-76;
Matches 206; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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RESULT 7
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 94.5%; Score 1057; DB 4; Length 236;
Best Local Similarity 94.9%; Pred. No. 7.7e-76;
Matches 205; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 8
US-09-456-090A-74
; Sequence 74, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-12L
US-09-456-090A-74

Query Match 94.4%; Score 1056; DB 4; Length 226;
Best Local Similarity 94.9%; Pred. No. 8.8e-76;
Matches 204; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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RESULT 9
US-09-453-234-74
; Sequence 74, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-12L
US-09-453-234-74

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Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
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RESULT 10
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-14

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              |||||||||||||||:|||||||||||||| |  :|||||||:|||||||||||||||
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Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 11
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-65

  Query Match             94.3%;  Score 1055.5;  DB 4;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 1e-75;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
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Qy         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
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Qy         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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Db         200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 12
US-09-456-090A-42
; Sequence 42, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-456-090A-42

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Db           1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy          61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
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Qy         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
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Db         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 13
US-09-453-234-42
; Sequence 42, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
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;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-453-234-42

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RESULT 14
US-09-859-053-38
; Sequence 38, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
;  APPLICANT: Tsuji, Takashi
;  APPLICANT:  Tezuka, Katsunari
;  APPLICANT:  Hori, No. 6803039uaki
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;  TITLE OF INVENTION:  COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;  TITLE OF INVENTION:  PHARMACEUTICAL USE THEREOF
;  FILE REFERENCE: 06501-079001
;  CURRENT APPLICATION NUMBER: US/09/859,053
;  CURRENT FILING DATE:  2001-05-16
;  PRIOR APPLICATION NUMBER: JP 2001-99508
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-859-053-38

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; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-25L
US-09-456-090A-52

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-684-957-33
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1068	95.4	226	10	US-09-453-234-80	Sequence 80, Appl
3	1068	95.4	226	10	US-09-453-234-86	Sequence 86, Appl
4	1065	95.2	226	10	US-09-453-234-50	Sequence 50, Appl
5	1057	94.5	236	9	US-09-859-053-34	Sequence 34, Appl
6	1057	94.5	236	16	US-10-625-105-34	Sequence 34, Appl
7	1057	94.5	236	18	US-10-800-250-34	Sequence 34, Appl
8	1056.5	94.4	215	15	US-10-307-724-122	Sequence 122, App
9	1056.5	94.4	215	16	US-10-737-290-122	Sequence 122, App
10	1056.5	94.4	239	16	US-10-737-290-142	Sequence 142, App
11	1056	94.4	226	10	US-09-453-234-74	Sequence 74, Appl
12	1056	94.4	236	17	US-10-910-901-8	Sequence 8, Appli
13	1055.5	94.3	235	14	US-10-153-382-7	Sequence 7, Appli
14	1055.5	94.3	235	16	US-10-612-497-14	Sequence 14, Appl
15	1055.5	94.3	235	16	US-10-612-497-65	Sequence 65, Appl
16	1055.5	94.3	235	16	US-10-776-649-14	Sequence 14, Appl
17	1055.5	94.3	235	16	US-10-776-649-65	Sequence 65, Appl
18	1055.5	94.3	384	15	US-10-291-265-804	Sequence 804, App
19	1055.5	94.3	384	15	US-10-291-265-805	Sequence 805, App
20	1055.5	94.3	384	15	US-10-291-265-806	Sequence 806, App
21	1055.5	94.3	384	15	US-10-291-265-807	Sequence 807, App
22	1053.5	94.1	235	17	US-10-938-353-60	Sequence 60, Appl
23	1053	94.1	226	10	US-09-453-234-42	Sequence 42, Appl
24	1052.5	94.1	215	18	US-10-916-758-16	Sequence 16, Appl
25	1049.5	93.8	235	17	US-10-938-353-32	Sequence 32, Appl
26	1048	93.7	236	9	US-09-859-053-38	Sequence 38, Appl
27	1048	93.7	236	16	US-10-625-105-38	Sequence 38, Appl
28	1048	93.7	236	18	US-10-800-250-38	Sequence 38, Appl
29	1046	93.5	234	15	US-10-292-088-88	Sequence 88, Appl
30	1045.5	93.4	235	17	US-10-938-353-44	Sequence 44, Appl
31	1045	93.4	224	10	US-09-453-234-52	Sequence 52, Appl
32	1044.5	93.3	235	15	US-10-180-648-4	Sequence 4, Appli
33	1044	93.3	226	10	US-09-453-234-38	Sequence 38, Appl
34	1043	93.2	226	10	US-09-453-234-72	Sequence 72, Appl
35	1041.5	93.1	215	17	US-10-684-957-18	Sequence 18, Appl
36	1041.5	93.1	215	17	US-10-684-957-22	Sequence 22, Appl
37	1039	92.9	224	10	US-09-453-234-76	Sequence 76, Appl
38	1039	92.9	234	14	US-10-153-382-15	Sequence 15, Appl
39	1039	92.9	234	16	US-10-612-497-17	Sequence 17, Appl
40	1039	92.9	234	16	US-10-612-497-69	Sequence 69, Appl
41	1039	92.9	234	16	US-10-776-649-17	Sequence 17, Appl
42	1039	92.9	234	16	US-10-776-649-69	Sequence 69, Appl
43	1036	92.6	224	10	US-09-453-234-44	Sequence 44, Appl
44	1036	92.6	224	10	US-09-453-234-78	Sequence 78, Appl
45	1034	92.4	224	10	US-09-453-234-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-684-957-33
; Sequence 33, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-ga
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-33

Query Match 100.0%; Score 1119; DB 17; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.3e-62;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60

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Qy          61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120

Qy         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
               |||||||||||||||||||||||||||||||||||
Db         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216


RESULT 2
US-09-453-234-80
; Sequence 80, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-20L
US-09-453-234-80

  Query Match             95.4%;  Score 1068;  DB 10;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 3.7e-59;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
               |||:||||||||||||||||||||||: |||||||||||| ||||||| | ||||||
Db           1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASRRATGIP 60

Qy          61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               ||||||||||||||||:||||||||||||:| ||||||||||||||||||||||||||||
Db          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPMYTFGQGTKLEIKRTVAAPSVFIF 120

Qy         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
               |||||||||||||||||||||||||||||||||
Db         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 3
US-09-453-234-86
; Sequence 86, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-33L
US-09-453-234-86

  Query Match             95.4%;  Score 1068;  DB 10;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 3.7e-59;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
               |||||||||||||||||||||||||||||: |||||||||||| ||||||| ||||||||
Db           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy          61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               ||||||||||||||||:||||||||||||:| ||||||||||||||||||||||||||||
Db          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
               |||||||||||||||||||||||||||||||||
Db         181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 4
US-09-453-234-50
; Sequence 50, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-23L
US-09-453-234-50

  Query Match             95.2%;  Score 1065;  DB 10;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 5.6e-59;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
               |||||||||||||||||||||||||||||: |||||||||||| ||||||| ||||||||
Db           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy          61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               ||||||||||||||||:||||||||||||:| ||||||||||||||||||||||||||||
Db          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120
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Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWRVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 5
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
;  APPLICANT: Tsuji, Takashi
;  APPLICANT:  Tezuka, Katsunari
;  APPLICANT:  Hori, No. US20020102658A1uaki
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;  TITLE OF INVENTION:  COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;  TITLE OF INVENTION:  PHARMACEUTICAL USE THEREOF
;  FILE REFERENCE: 06501-079001
;  CURRENT APPLICATION NUMBER: US/09/859,053
;  CURRENT FILING DATE:  2001-05-16
;  PRIOR APPLICATION NUMBER: JP 2001-99508
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-859-053-34

  Query Match             94.5%;  Score 1057;  DB 9;  Length 236;
  Best Local Similarity   94.9%;  Pred. No. 1.8e-58;
  Matches  205;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||:| |||||||||||| | ||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAWYQQKPGQAPGLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||:|:| | :||||||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 6
US-10-625-105-34
; Sequence 34, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
;  APPLICANT: Tsuji, Takashi
;  APPLICANT:  Tezuka, Katsunari
;  APPLICANT:  Hori, Nobuaki
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;  TITLE OF INVENTION:  COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;  TITLE OF INVENTION:  PHARMACEUTICAL USE THEREOF
;  FILE REFERENCE: 06501-079001
;  CURRENT APPLICATION NUMBER: US/10/625,105
;  CURRENT FILING DATE:  2003-07-22
;  PRIOR APPLICATION NUMBER: US/09/859,053
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: JP 2001-99508
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-625-105-34

  Query Match             94.5%;  Score 1057;  DB 16;  Length 236;
  Best Local Similarity   94.9%;  Pred. No. 1.8e-58;
  Matches  205;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||:| |||||||||||| | ||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAWYQQKPGQAPGLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||:|:| | :||||||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 7
US-10-800-250-34
; Sequence 34, Application US/10800250
; Publication No. US20040146991A1
; GENERAL INFORMATION:
;  APPLICANT: Tsuji, Takashi
;  APPLICANT:  Tezuka, Katsunari
;  APPLICANT:  Hori, Nobuaki
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;  TITLE OF INVENTION:  COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;  TITLE OF INVENTION:  PHARMACEUTICAL USE THEREOF
;  FILE REFERENCE: 06501-079001
;  CURRENT APPLICATION NUMBER: US/10/800,250
;  CURRENT FILING DATE:  2004-03-10
;  PRIOR APPLICATION NUMBER: US/09/859,053
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: JP 2001-99508
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-800-250-34

  Query Match             94.5%;  Score 1057;  DB 18;  Length 236;
  Best Local Similarity   94.9%;  Pred. No. 1.8e-58;
  Matches  205;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||:| |||||||||||| | ||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAWYQQKPGQAPGLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||:|:| | :||||||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 8
US-10-307-724-122
; Sequence 122, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2cip
;  CURRENT APPLICATION NUMBER: US/10/307,724
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 134
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antibody light chain
US-10-307-724-122

  Query Match             94.4%;  Score 1056.5;  DB 15;  Length 215;
  Best Local Similarity   94.9%;  Pred. No. 1.8e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||: ||||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:||||||||||||||:|  :|||||||:||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PWTFGQGTKVEIKRTVAAPSVFIF 119

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||| ||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 215


RESULT 9
US-10-737-290-122
; Sequence 122, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  APPLICANT:  Orencia, Cecilia
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2 CIP III
;  CURRENT APPLICATION NUMBER: US/10/737,290
;  CURRENT FILING DATE:  2003-12-15
;  PRIOR APPLICATION NUMBER: US 10/452,590
;  PRIOR FILING DATE: 2003-06-02
;  PRIOR APPLICATION NUMBER: US 10/307,724
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antibody light chain
US-10-737-290-122

  Query Match             94.4%;  Score 1056.5;  DB 16;  Length 215;
  Best Local Similarity   94.9%;  Pred. No. 1.8e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||: ||||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:||||||||||||||:|  :|||||||:||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PWTFGQGTKVEIKRTVAAPSVFIF 119

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||| ||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 215


RESULT 10
US-10-737-290-142
; Sequence 142, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  APPLICANT:  Orencia, Cecilia
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2 CIP III
;  CURRENT APPLICATION NUMBER: US/10/737,290
;  CURRENT FILING DATE:  2003-12-15
;  PRIOR APPLICATION NUMBER: US 10/452,590
;  PRIOR FILING DATE: 2003-06-02
;  PRIOR APPLICATION NUMBER: US 10/307,724
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: artificial sequence
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;   FEATURE:
;   OTHER INFORMATION: recombinant Ab light chain
US-10-737-290-142

  Query Match             94.4%;  Score 1056.5;  DB 16;  Length 239;
  Best Local Similarity   94.9%;  Pred. No. 2e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||||||: |||||||||||||| ||||||| ||||||||
Db         25 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 84

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
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Db         85 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PWTFGQGTKVEIKRTVAAPSVFIF 143

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
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Db        144 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 203

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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Db        204 LTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 239


RESULT 11
US-09-453-234-74
; Sequence 74, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-12L
US-09-453-234-74

  Query Match             94.4%;  Score 1056;  DB 10;  Length 226;
  Best Local Similarity   94.9%;  Pred. No. 2e-58;
  Matches  204;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:||||||||||||||||||||| : |||||||||||||| ||||||| ||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||: ||||||||||||||:|  ||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
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Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 12
US-10-910-901-8
; Sequence 8, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
;  APPLICANT: MICHAUD, NEIL R., et al.
;  TITLE OF INVENTION: ANTIBODIES TO c-MET
;  FILE REFERENCE: ABX-PF5
;  CURRENT APPLICATION NUMBER: US/10/910,901
;  CURRENT FILING DATE:  2004-08-03
;  PRIOR APPLICATION NUMBER: US 60/492,432
;  PRIOR FILING DATE: 2003-08-04
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-910-901-8

  Query Match             94.4%;  Score 1056;  DB 17;  Length 236;
  Best Local Similarity   94.0%;  Pred. No. 2.1e-58;
  Matches  203;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||||: ::|||||||||||| ||||:| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPRLLIFGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||:|||||||||||||   | ||:||||||||:||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDISPMYSFGQGTKLEMKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 13
US-10-153-382-7
; Sequence 7, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-153-382-7

  Query Match             94.3%;  Score 1055.5;  DB 14;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 2.3e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||| ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||:|||||||||||||||| |  :|||||||:||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS-PWTFGQGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
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Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
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Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 14
US-10-612-497-14
; Sequence 14, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV1
;  CURRENT APPLICATION NUMBER: US/10/612,497
;  CURRENT FILING DATE:  2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-612-497-14

  Query Match             94.3%;  Score 1055.5;  DB 16;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 2.3e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||| ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||||| |  :|||||||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS-PWTFGQGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 15
US-10-612-497-65
; Sequence 65, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV1
;  CURRENT APPLICATION NUMBER: US/10/612,497
;  CURRENT FILING DATE:  2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-612-497-65

  Query Match             94.3%;  Score 1055.5;  DB 16;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 2.3e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||| ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||||| |  :|||||||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS-PWTFGQGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


Search completed: September  8, 2005, 00:48:35
Job time : 54.7962 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:15:52 ; Search time 52.4921 Seconds
(without alignments)
2107.158 Million cell updates/sec

Title: US-10-684-957-33
Perfect score: 1119
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1059	94.6	236	2	Q6PIL8	Q6pil8 homo sapien
2	1043	93.2	236	2	Q6P5S8	Q6p5s8 homo sapien
3	1026.5	91.7	235	2	Q6PJF2	Q6pjf2 homo sapien
4	1012.5	90.5	235	2	Q6GMV9	Q6gmv9 homo sapien
5	998.5	89.2	235	2	Q6GMW0	Q6gmw0 homo sapien
6	932	83.3	236	2	Q6GMX8	Q6gmx8 homo sapien
7	927	82.8	236	2	Q7Z3Y4	Q7z3y4 homo sapien
8	922	82.4	236	2	Q6PIH7	Q6pih7 homo sapien
9	922	82.4	240	2	Q6PIH6	Q6pih6 homo sapien
10	919	82.1	236	2	Q6PIT5	Q6pit5 homo sapien
11	916	81.9	234	2	Q7Z473	Q7z473 homo sapien
12	914	81.7	236	2	Q6GMW1	Q6gmw1 homo sapien
13	914	81.7	236	2	Q6GMX9	Q6gmx9 homo sapien
14	909	81.2	236	2	Q6PIH4	Q6pih4 homo sapien
15	904.5	80.8	239	2	Q8NEK0	Q8nek0 homo sapien
16	903.5	80.7	239	2	Q8TCD0	Q8tcd0 homo sapien
17	898	80.3	236	2	Q6GMX0	Q6gmx0 homo sapien
18	883.5	79.0	239	2	Q6P491	Q6p491 homo sapien
19	699.5	62.5	219	2	Q65ZC0	Q65zc0 mus musculu
20	683	61.0	238	2	Q66JS7	Q66js7 mus musculu
21	674	60.2	236	2	Q7TS98	Q7ts98 mus musculu
22	653	58.4	241	2	Q63ZX4	Q63zx4 mus musculu
23	605	54.1	120	2	Q6P5R5	Q6p5r5 homo sapien
24	575	51.4	237	2	Q7SZ36	Q7sz36 xenopus lae
25	574.5	51.3	243	2	Q6NTU5	Q6ntu5 xenopus lae
26	548	49.0	106	1	KAC_HUMAN	P01834 homo sapien
27	509.5	45.5	129	1	KV3L_HUMAN	P18135 homo sapien
28	508.5	45.4	129	1	KV3M_HUMAN	P18136 homo sapien
29	501.5	44.8	109	1	KV3B_HUMAN	P01620 homo sapien
30	500.5	44.7	109	1	KV3E_HUMAN	P01623 homo sapien
31	497.5	44.5	109	2	Q9UL78	Q9ul78 homo sapien
32	495.5	44.3	109	2	Q9UL86	Q9ul86 homo sapien
33	492.5	44.0	109	1	KV3D_HUMAN	P01622 homo sapien
34	487.5	43.6	108	1	KV3A_HUMAN	P01619 homo sapien
35	473.5	42.3	109	1	KV3G_HUMAN	P04206 homo sapien
36	468	41.8	236	2	Q6GMX4	Q6gmx4 homo sapien
37	463	41.4	100	1	KV3C_HUMAN	P01621 homo sapien
38	461.5	41.2	235	2	Q6IN99	Q6in99 homo sapien
39	458	40.9	236	2	Q6IPQ0	Q6ipq0 homo sapien
40	457	40.8	128	1	KV3K_HUMAN	P06311 homo sapien
41	456	40.8	236	2	Q8NEJ1	Q8nej1 homo sapien
42	452.5	40.4	233	2	Q8TBC9	Q8tbc9 homo sapien
43	451.5	40.3	129	1	KV3H_HUMAN	P04207 homo sapien
44	449	40.1	236	2	Q6PIQ7	Q6piq7 homo sapien
45	447.5	40.0	235	2	Q6PIK1	Q6pik1 homo sapien

ALIGNMENTS

RESULT 1
Q6PIL8
ID Q6PIL8 PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

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KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match           94.6%;  Score 1059;  DB 2;  Length 236;
  Best Local Similarity   94.9%;  Pred. No. 6.2e-83;
  Matches  205;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              | ||||||||||||||||||||||||: |||||||||||| ||||||||||||||||
Db         21 ENVLTQSPGTLSLSPGERATLSCRASQSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||:|||||||||||||||| |   ||||||:|:||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
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Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 2
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match           93.2%;  Score 1043;  DB 2;  Length 236;
  Best Local Similarity   92.6%;  Pred. No. 1.5e-81;
  Matches  200;  Conservative    7;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||| ||||||||||||:: ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSFSPGERATLSCRASQTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||||||||||:||||| |   ||| ||::|||||||||||||||
Db         81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQQYGTSPSLTFGGGTRVEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 3
Q6PJF2
ID   Q6PJF2      PRELIMINARY;      PRT;   235 AA.
AC   Q6PJF2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016380; AAH16380.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match             91.7%;  Score 1026.5;  DB 2;  Length 235;
  Best Local Similarity   92.1%;  Pred. No. 3.8e-80;
  Matches  199;  Conservative    8;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||| |||||||||||||||||| : |:|||||||||| ||||::| ||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||:|||||||||||||||:|   ||| |||::|||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-QGTFGPGTKVDIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 4
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             90.5%;  Score 1012.5;  DB 2;  Length 235;
  Best Local Similarity   91.2%;  Pred. No. 6.1e-79;
  Matches  197;  Conservative    7;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||| |||||||: | |||||||||| ||||:|  | ||||||
Db         21 EIVLTQSPGTLSLSPGERAALSCRASQSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||:||| ||||:|:||||| | : ||| |||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGTSPL-TFGGGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 5
Q6GMW0
ID   Q6GMW0      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMW0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
```

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RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073792; AAH73792.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25765 MW;  4360C36B6D4133F5 CRC64;

  Query Match             89.2%;  Score 998.5;  DB 2;  Length 235;
  Best Local Similarity   89.4%;  Pred. No. 9.8e-78;
  Matches  193;  Conservative   11;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:|||| |||:|||||||||||||||| ||: ||||||:||| ||||||| ||| ||||
Db         21 EIVMTQSPATLSVSPGERATLSCRASQS-ISNNLAWYQQRPGQAPRLLIYGASSRVTGIP 79

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               |||||||||:|||:|: |: ||||||:|||| :  :|||||||||||||||||||||||
Db         80 GRFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWLLYTFGQGTKLEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 6
Q6GMX8
ID   Q6GMX8      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match             83.3%;  Score 932;  DB 2;  Length 236;
  Best Local Similarity   82.9%;  Pred. No. 5.1e-72;
  Matches  179;  Conservative   18;  Mismatches   17;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              :| :|||| ::| | |:| |::||||| |||:|||||||||: |:|||| || :|:|
Db         23 DIQMTQSPSSVSASVGDRVTITCRASQG-ISSWLAWYQQKPGKAPKLLIYAASSLQSGVP 81

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               |||||||||||||: |:||||| |||||  :|| :||| |||::|||||||||||||
Db         82 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQ-AHSFPFTFGPGTKVDIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 7
Q7Z3Y4
ID   Q7Z3Y4      PRELIMINARY;      PRT;   236 AA.
AC   Q7Z3Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25702 MW;  7FBFE4ED23084BC6 CRC64;

  Query Match             82.8%;  Score 927;  DB 2;  Length 236;
  Best Local Similarity   82.9%;  Pred. No. 1.4e-71;
  Matches  179;  Conservative   16;  Mismatches   19;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              :| :|||| :|| | |:  |::|||||  ||:||||:|||||: |: |||| ||  :|:
Db         23 DIQMTQSPSSLSASVGDTVTITCRASQD-ISNYLAWFQQKPGKAPKSLIYGASSLQSGVQ 81

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
               :|||||||||||||: |:||||| |||||  |:  ||||||||||||||||||||||
Db         82 SKFSGSGSGTDFTLTISSLQPEDFATYYCQQY-KSYPVTFGQGTKLEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 8
Q6PIH7
ID   Q6PIH7      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25603 MW;  8BC561106861213F CRC64;

  Query Match             82.4%;  Score 922;  DB 2;  Length 236;
  Best Local Similarity   83.8%;  Pred. No. 3.7e-71;
  Matches  181;  Conservative   12;  Mismatches   21;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              :| |||||  || | |:| |::|||||  ||||||||||||: | ||||  |:  :|:|
Db         23 DIQLTQSPSFLSASVGDRVTITCRASQG-ISSYLAWYQQKPGKAPNLLIYAASTLQSGVP 81

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||:|||||: |:||||| |||||  ||   ||| |||:|||||||||||||
Db         82 SRFSGSGSGTEFTLTISSLQPEDFATYYCQQL-NSSPPTFGGGTKVEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 9
Q6PIH6
ID   Q6PIH6      PRELIMINARY;      PRT;   240 AA.
AC   Q6PIH6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
```

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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034142; AAH34142.1; -.
DR   HSSP; P01837; 1KB5.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   240 AA;  26234 MW;  188D4DD8BB781EC4 CRC64;

  Query Match             82.4%;  Score 922;  DB 2;  Length 240;
  Best Local Similarity   81.4%;  Pred. No. 3.8e-71;
  Matches  179;  Conservative   18;  Mismatches   19;  Indels    4;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS----YLAWYQQKPGQTPRLLIYGVSSRA 56
              :||: ||| :||::||| |::|||:|||:: |     |  || |||||:|:||||  |:||
Db         21 DIVMAQSPLSLSVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYWGSNRA 80

Qy         57 TGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPS 116
              :|:|||||||||||||| |:|:| ||  |||| |   :  ||||||||||||||||||
Db         81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPYTFGQGTKLEIKRTVAAPS 140

Qy        117 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 200

Qy        177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||||
Db        201 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240


RESULT 10
Q6PIT5
ID   Q6PIT5      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIT5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029444; AAH29444.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25741 MW;  BD50AF071FEEE351 CRC64;

  Query Match             82.1%;  Score 919;  DB 2;  Length 236;
  Best Local Similarity   83.7%;  Pred. No. 6.7e-71;
  Matches  180;  Conservative   13;  Mismatches   20;  Indels    2;  Gaps    2;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIPD 61
              | ||||| :|| | ||| |::|||||  ||| |||||||||: |:||||  |:  :|:|
Db         24 IQLTQSPSSLSASVGERVTITCRASQG-ISSALAWYQQKPGKPPKLLIYDASTMESGVPS 82

Qy         62 RFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIFP 121
              ||||||||| ||||| |:|||||  :||||:  |:  ||||||  ||||||||||||||||
Db         83 RFSGSGSGTHFTLTISSLQPEDFATFYCQQF-KSYPRTFGQGTTLEIKRTVAAPSVFIFP 141

Qy        122 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        182 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 11
Q7Z473
ID   Q7Z473      PRELIMINARY;      PRT;   234 AA.
AC   Q7Z473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

  Query Match             81.9%;  Score 916;  DB 2;  Length 234;
  Best Local Similarity   82.3%;  Pred. No. 1.2e-70;
  Matches  177;  Conservative   17;  Mismatches   19;  Indels    2;  Gaps    2;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIPD 61
              | :|||| : | | |:| |::|||||| | |||||||||||: |:|||| |:  :|:|
Db         22 IRMTQSPSSFSASTGDRVTITCRASQS-IGSYLAWYQQKPGKAPQLLIYAASTLQSGVPS 80

Qy         62 RFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIFP 121
              ||||| |||||||:|: |: |||| |||||  :: :||||||:|||||||||||||||
Db         81 RFSGSASGTDFTLSISCLQSEDFATYYCQQY-YTYPWTFGQGTKVEIKRTVAAPSVFIFP 139

Qy        122 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 199

Qy        182 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 12
Q6GMW1
ID   Q6GMW1      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             81.7%;  Score 914;  DB 2;  Length 236;
  Best Local Similarity   82.8%;  Pred. No. 1.8e-70;
  Matches  178;  Conservative   15;  Mismatches   20;  Indels    2;  Gaps    2;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIPD 61
              | :|||| :|| | |:| |::|||||  ||: | ||||||||: |:|||||  ||  :|:|
Db         24 IQMTQSPSSLSASVGDRVTITCRASQG-ISNDLGWYQQKPGKAPKLLIYAASSLQSGVPS 82

Qy         62 RFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIFP 121
              |||||||||||||||: |:||||| ||| |  | : :|||||||:||||||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCLQDYN-YPWTFGQGTKVEIKRTVAAPSVFIFP 141

Qy        122 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        182 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 13
Q6GMX9
ID   Q6GMX9      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073763; AAH73763.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25924 MW;  FDE2093DC560CFF7 CRC64;

  Query Match             81.7%;  Score 914;  DB 2;  Length 236;
  Best Local Similarity   81.5%;  Pred. No. 1.8e-70;
  Matches  176;  Conservative   18;  Mismatches   20;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              :| :|||| :|| | | | |::|||||: :| :||||||:| : |: |||  ||  :|:|
Db         23 DIQMTQSPSSLSASVGHRVTITCRASQN-VSRWLAWYQQRPEKAPKSLIYATSSLHSGVP 81

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
                |||||||||||||||: |:||||| |||||| |::  ||| |||:|||||||||||||
Db         82 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQY-NTYPLTFGGGTKVEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              ||||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 14
Q6PIH4
ID   Q6PIH4      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034146; AAH34146.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25871 MW;  BE01A28CD06EEE26 CRC64;

  Query Match             81.2%;  Score 909;  DB 2;  Length 236;
  Best Local Similarity   81.9%;  Pred. No. 4.9e-70;
  Matches  177;  Conservative   16;  Mismatches   21;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              :| :|||| ||| | |:| |::|||||  || :|||||||: |:||||  |   :|:|
Db         23 DIQMTQSPSTLSASVGDRVTIACRASQ-WISDWLAWYQQKPGKAPKLLIYDASRLESGVP 81

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
                |||||||||:|:|||: |:|:||| |||| | ||    ||||||:|||||||||||||
Db         82 SRFSGSGSGTEFSLTISGLQPDDFATYYCQPY-NSNSPQFGQGTKVEIKRTVAAPSVFIF 140
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Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 15
Q8NEK0
ID   Q8NEK0      PRELIMINARY;      PRT;   239 AA.
AC   Q8NEK0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030814; AAH30814.1; -.
DR   PIR; S23638; S23638.
DR   PIR; S34091; S34091.
DR   PIR; S40342; S40342.
DR   PIR; S40357; S40357.
DR   HSSP; P01834; 1I7Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   239 AA;  26024 MW;  F5E20AD3B0552C0A CRC64;

  Query Match           80.8%;  Score 904.5;  DB 2;  Length 239;
  Best Local Similarity  80.0%;  Pred. No. 1.2e-69;
  Matches  176;  Conservative   20;  Mismatches   19;  Indels    5;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS----YLAWYQQKPGQTPRLLIYGVSSRA 56
              :||:|||| :| ::||| |::|||:|||:: |    || || |||||:|:||||  |:||
Db         21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA 80

Qy         57 TGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPS 116
              :|:|||||||||||||| |:::| ||  :||| | |     ||||||||:|||||||||
Db         81 SGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQ-GLQTPQTFGQGTKVEIKRTVAAPS 139

Qy        117 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 176
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNTLQSGNSQESVTEQDSKDSTYS 199

Qy        177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||||
Db        200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239


Search completed: September  8, 2005, 00:54:04
Job time : 53.4921 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:11:22 ; Search time 58.1977 Seconds
(without alignments)
1435.455 Million cell updates/sec

Title: US-10-684-957-33
Perfect score: 1119
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1119	100.0	216	8	ADS87940	Ads87940 Anti-IFN-
2	1119	100.0	216	8	ADS94937	Ads94937 Anti-IFN-
3	1068	95.4	226	4	AAB99397	Aab99397 Human int
4	1068	95.4	226	4	AAB99394	Aab99394 Human int
5	1068	95.4	226	4	AAB75027	Aab75027 Anti-IL8
6	1068	95.4	226	4	AAB75030	Aab75030 Anti-IL8
7	1065	95.2	226	4	AAB99374	Aab99374 Human int
8	1065	95.2	226	4	AAB75007	Aab75007 Anti-IL8
9	1057	94.5	236	5	AAU74299	Aau74299 Anti-huma
10	1056.5	94.4	215	8	ADQ16702	Adq16702 Modified
11	1056	94.4	226	4	AAB99391	Aab99391 Human int
12	1056	94.4	226	4	AAB75024	Aab75024 Anti-IL8
13	1055.5	94.3	235	3	AAY93702	Aay93702 The kappa
14	1055.5	94.3	235	3	AAY93729	Aay93729 The kappa
15	1055.5	94.3	235	6	AAE35884	Aae35884 Human 4.1
16	1055.5	94.3	384	4	AAU14462	Aau14462 Human nov
17	1055.5	94.3	384	4	AAU14463	Aau14463 Human nov
18	1055.5	94.3	384	4	AAU14461	Aau14461 Human nov
19	1055.5	94.3	384	4	AAU14464	Aau14464 Human nov
20	1055.5	94.3	384	8	ADH80782	Adh80782 Human pol
21	1053.5	94.1	384	8	ADH80779	Adh80779 Human pol
22	1053.5	94.1	384	8	ADH80781	Adh80781 Human pol
23	1053.5	94.1	385	8	ADH80780	Adh80780 Human pol
24	1053	94.1	226	4	AAB99378	Aab99378 Human int
25	1053	94.1	226	4	AAB75011	Aab75011 Anti-IL8
26	1048	93.7	236	5	AAU74301	Aau74301 Anti-huma
27	1047	93.6	214	8	ADP73860	Adp73860 Human ant
28	1047	93.6	233	8	ADP73856	Adp73856 Human ant
29	1046	93.5	234	7	ADE28481	Ade28481 Human ant
30	1045	93.4	224	4	AAB99375	Aab99375 Human int
31	1045	93.4	224	4	AAB75008	Aab75008 Anti-IL8
32	1044.5	93.3	235	6	ABP71366	Abp71366 Anti-OPGL
33	1044	93.3	226	4	AAB99376	Aab99376 Human int
34	1044	93.3	226	4	AAB75009	Aab75009 Anti-IL8
35	1043	93.2	226	4	AAB99390	Aab99390 Human int
36	1043	93.2	226	4	AAB75023	Aab75023 Anti-IL8
37	1041.5	93.1	215	8	ADS87929	Ads87929 Anti-IFN-
38	1041.5	93.1	215	8	ADS87925	Ads87925 Anti-IFN-
39	1041.5	93.1	215	8	ADS94926	Ads94926 Anti-IFN-
40	1041.5	93.1	215	8	ADS94922	Ads94922 Anti-IFN-
41	1039	92.9	224	4	AAB99392	Aab99392 Human int
42	1039	92.9	224	4	AAB75025	Aab75025 Anti-IL8
43	1039	92.9	234	3	AAY93733	Aay93733 The kappa
44	1039	92.9	234	3	AAY93708	Aay93708 The kappa
45	1039	92.9	234	6	AAE35888	Aae35888 Human 6.1

ALIGNMENTS

RESULT 1
ADS87940
ID ADS87940 standard; protein; 216 AA.
XX
AC ADS87940;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121* light chain SEQ ID NO:33.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 33; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36

CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 1119; DB 8; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.7e-62;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
```

RESULT 2
ADS94937
ID ADS94937 standard; protein; 216 AA.
XX
AC ADS94937;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121* light chain SEQ ID NO:33.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 33; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 1119; DB 8; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.7e-62;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
```

RESULT 3
AAB99397
ID AAB99397 standard; protein; 226 AA.
XX
AC AAB99397;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody protein sequence M2_33L.
XX
KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX

```
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033042.
XX
PR   06-DEC-1999;   99US-00456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding to
PT   nonhuman-antibodies, involves contacting sample with human antibody which
PT   binds to antibodies from nonhuman species and detecting binding.
XX
PS   Example 22; Page 96; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the amount
CC   of target antigen in a sample in a semi-quantitative or relative sense.
CC   Quantification of one or more target antigens in a sample can also be
CC   carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 226 AA;

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 2.7e-59;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||||: |||||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:||||||||||||||||:|  ||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 4
AAB99394
ID   AAB99394 standard; protein; 226 AA.
XX
AC   AAB99394;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Human interleukin 8 antibody protein sequence M2_20L.
XX
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033042.
XX
PR   06-DEC-1999;   99US-00456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding to
PT   nonhuman-antibodies, involves contacting sample with human antibody which
PT   binds to antibodies from nonhuman species and detecting binding.
XX
PS   Example 22; Page 96; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the amount
CC   of target antigen in a sample in a semi-quantitative or relative sense.
CC   Quantification of one or more target antigens in a sample can also be
CC   carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 226 AA;

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 2.7e-59;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:|||||||||||||||||||||||: |||||||||||| ||||||| | ||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASRRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||||:| ||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPMYTFGQGTKLEIKRTVAAPSVFIF 120
```

```
Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 5
AAB75027
ID   AAB75027 standard; protein; 226 AA.
XX
AC   AAB75027;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody protein fragment M2_20L.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027237.
XX
PR   02-OCT-1999;   99US-0157415P.
PR   01-DEC-1999;   99US-00453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS   Example 22; Page 99-100; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 226 AA;

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 2.7e-59;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:|||||||||||||||||||||: |||||||||||| ||||||| | ||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASRRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||||:| |||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPMYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 6
AAB75030
ID   AAB75030 standard; protein; 226 AA.
XX
AC   AAB75030;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody protein fragment M2_33L.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027237.
XX
PR   02-OCT-1999;   99US-0157415P.
PR   01-DEC-1999;   99US-00453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS   Example 22; Page 99-100; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 226 AA;

  Query Match             95.4%;  Score 1068;  DB 4;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 2.7e-59;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||: |||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:||||||||||||||:|  ||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
```

RESULT 7
AAB99374
ID AAB99374 standard; protein; 226 AA.
XX
AC AAB99374;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody protein sequence M1_23L.
XX
KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200140306-A1.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US033042.
XX
PR 06-DEC-1999; 99US-00456090.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR WPI; 2001-374798/39.
XX
PT Detecting analyte in human sample containing human antibodies binding to
PT nonhuman-antibodies, involves contacting sample with human antibody which
PT binds to antibodies from nonhuman species and detecting binding.
XX
PS Example 22; Page 94; 135pp; English.
XX
CC The present invention describes a method for detecting an analyte in a
CC human sample containing human antibodies that specifically bind to
CC antibodies from a nonhuman species. The method involves contacting the
CC sample with a human antibody (I) which specifically binds to antibodies
CC from a nonhuman species and detecting the binding between (I) and the
CC analyte to indicate presence of the analyte. The method is used for
CC detecting an analyte in a human sample containing human anti-mouse
CC antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC heterophilic antibodies). The method can also be used for detecting any
CC type of target antigen including bacterial, fungal and viral pathogens
CC that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC aeruginosa. Human antibodies can be used as detection reagents for
CC performing clinical diagnostic tests and for performing other in vitro
CC detection assays, including for research purposes. (I) can be used in
CC qualitative assays designed to indicate the presence of one or more
CC target antigens above minimally detectable amounts of antigen in the
CC sample that usually correspond to the sensitivity limitations of the
CC assays for each target antigen. Also, (I) is used to determine the amount
CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 226 AA;

```
  Query Match             95.2%;  Score 1065;  DB 4;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 4.2e-59;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||: |||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:||||||||||||||:|  ||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWRVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
```

RESULT 8
AAB75007
ID AAB75007 standard; protein; 226 AA.
XX
AC AAB75007;
XX
DT 19-JUL-2001 (first entry)
XX
DE Anti-IL8 monoclonal antibody protein fragment M1_23L.
XX
KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200125492-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-US027237.
XX
PR 02-OCT-1999; 99US-0157415P.
PR 01-DEC-1999; 99US-00453234.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR WPI; 2001-335567/35.
XX
PT Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS Example 22; Page 98; 161pp; English.
XX
CC The present invention describes a method (M1) for producing a human
CC antibody phage display library (I), comprising: (1) providing a nonhuman
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC (2) isolating nucleic acids encoding human antibody chains (III) from

```
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 226 AA;

  Query Match             95.2%;  Score 1065;  DB 4;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 4.2e-59;
  Matches  206;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||: ||||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:||||||||||||||:|  ||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWRVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 9
AAU74299
ID   AAU74299 standard; protein; 236 AA.
XX
AC   AAU74299;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
XX
KW   Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
KW   immunosuppressive; dermatological; antiinflammatory; hepatotropic;
KW   activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW   monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW   multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW   allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW   systemic lupus erythematosus; autoimmune disorder; inflammation;
KW   graft versus host reaction; immune rejection; intestinal immunity;
KW   ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX
OS   Homo sapiens.
XX
PN   WO200187981-A2.
XX
PD   22-NOV-2001.
XX
PF   15-MAY-2001; 2001WO-JP004035.
XX
PR   18-MAY-2000; 2000JP-00147116.
PR   30-MAR-2001; 2001JP-00099508.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Tsuji T,  Tezuka K,  Hori N;
XX
DR   WPI; 2002-075313/10.
DR   N-PSDB; AAS99475.
XX
PT   New human monoclonal antibody that binds to activation inducible
PT   lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT   arthritis, multiple sclerosis and inflammation.
XX
PS   Claim 30; Page 284-285; 300pp; English.
XX
CC   The invention relates to a novel human antibody (I), preferably a human
CC   monoclonal antibody which binds to an activation inducible lymphocyte
CC   immunomodulatory molecule (AILIM). (I) is useful for modulating signal
CC   transduction into a cell mediated by AILIM, for modulating proliferation
CC   of AILIM-expressing cells, for modulating production of a cytokine from
CC   AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC   against AILIM-expressing cells and/or immune cytolysis or apoptosis of
CC   AILIM-expressing cells. (I) is useful for treating, preventing or
CC   prophylaxis of delayed type allergy. (I) is useful for treating and
CC   preventing various diseases associated with AILIM-mediated costimulatory
CC   transduction, and for inhibiting the onset and/or advancement of the
CC   diseases. (I) is useful for suppression, prevention and/or treatment of
CC   rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC   allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC   systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC   psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC   host reaction, graft versus host disease, immune rejection, disorders
CC   caused by abnormal intestinal immunity, specifically inflammatory
CC   intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC   nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC   immunorejection due to antigenicity to human, i.e., human anti-mouse
CC   antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
CC   AILIM monoclonal antibody amino acid sequences of the invention
XX
SQ   Sequence 236 AA;

  Query Match             94.5%;  Score 1057;  DB 5;  Length 236;
  Best Local Similarity   94.9%;  Pred. No. 1.4e-58;
  Matches  205;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||:| |||||||||||| | ||||| |||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAWYQQKPGQAPGLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||:|:| | :||||||||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIKRTVAAPSVFIF 140

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 10
ADQ16702
ID   ADQ16702 standard; protein; 215 AA.
XX
AC   ADQ16702;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Modified immunoglobuiln clone 116 light chain SEQ ID NO:122.
XX
KW   immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KW   erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW   immunotherapy; thrombocytopenia.
XX
OS   Synthetic.
XX
PN   WO2004050017-A2.
XX
PD   17-JUN-2004.
```

XX
PF 17-NOV-2003; 2003WO-US036894.
XX
PR 02-DEC-2002; 2002US-00307724.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Renshaw M;
XX
DR WPI; 2004-460973/43.
XX
PT New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
PS Example 8; SEQ ID NO 122; 107pp; English.
XX
CC The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents immunoglobulin clone 116 light chain.
XX
SQ Sequence 215 AA;

Query Match 94.4%; Score 1056.5; DB 8; Length 215;
Best Local Similarity 94.9%; Pred. No. 1.4e-58;
Matches 205; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||||: ||||||||||||| ||||||| ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||:||||||||||||||:|  :|||||||:|||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PWTFGQGTKVEIKRTVAAPSVFIF 119

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||| ||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 215
```

RESULT 11
AAB99391
ID AAB99391 standard; protein; 226 AA.
XX
AC AAB99391;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody protein sequence M2_12L.
XX
KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200140306-A1.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US033042.
XX
PR 06-DEC-1999; 99US-00456090.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR WPI; 2001-374798/39.
XX
PT Detecting analyte in human sample containing human antibodies binding to
PT nonhuman-antibodies, involves contacting sample with human antibody which
PT binds to antibodies from nonhuman species and detecting binding.
XX
PS Example 22; Page 95-96; 135pp; English.
XX
CC The present invention describes a method for detecting an analyte in a
CC human sample containing human antibodies that specifically bind to
CC antibodies from a nonhuman species. The method involves contacting the
CC sample with a human antibody (I) which specifically binds to antibodies
CC from a nonhuman species and detecting the binding between (I) and the
CC analyte to indicate presence of the analyte. The method is used for
CC detecting an analyte in a human sample containing human anti-mouse
CC antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC heterophilic antibodies). The method can also be used for detecting any
CC type of target antigen including bacterial, fungal and viral pathogens
CC that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC aeruginosa. Human antibodies can be used as detection reagents for
CC performing clinical diagnostic tests and for performing other in vitro
CC detection assays, including for research purposes. (I) can be used in
CC qualitative assays designed to indicate the presence of one or more
CC target antigens above minimally detectable amounts of antigen in the
CC sample that usually correspond to the sensitivity limitations of the
CC assays for each target antigen. Also, (I) is used to determine the amount
CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 226 AA;

Query Match 94.4%; Score 1056; DB 4; Length 226;
Best Local Similarity 94.9%; Pred. No. 1.5e-58;
Matches 204; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:|||||||||||||||||||||||| : |||||||||||||| ||||||| ||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||: ||||||||||||||:|  ||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
```

RESULT 12
AAB75024
ID AAB75024 standard; protein; 226 AA.
XX
AC AAB75024;
XX
DT 19-JUL-2001 (first entry)
XX

```
DE   Anti-IL8 monoclonal antibody protein fragment M2_12L.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027237.
XX
PR   02-OCT-1999;   99US-0157415P.
PR   01-DEC-1999;   99US-00453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS   Example 22; Page 99-100; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 226 AA;

  Query Match             94.4%;  Score 1056;  DB 4;  Length 226;
  Best Local Similarity   94.9%;  Pred. No. 1.5e-58;
  Matches  204;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:||||||||||||||||||||| : |||||||||||| ||||||| ||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||: |||||||||||||||:|  ||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIKRTVAAPSVFIF 120

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 13
AAY93702
ID   AAY93702 standard; protein; 235 AA.
XX
AC   AAY93702;
XX
DT   03-OCT-2000  (first entry)
XX
DE   The kappa chain of immunoglobulin clone 4.1.1.
XX
KW   Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW   hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW   proliferative disorder; cancer; immunodeficient disorder.
XX
OS   Homo sapiens.
XX
PN   WO200037504-A2.
XX
PD   29-JUN-2000.
XX
PF   23-DEC-1999;   99WO-US030895.
XX
PR   23-DEC-1998;   98US-0113647P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Hanson DC,  Neveu MJ,  Mueller EE,  Hanke JH,  Gilman SC,  Davis CG;
PI   Corvalan JR;
XX
DR   WPI; 2000-442647/38.
DR   N-PSDB; AAA46865.
XX
PT   Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT   -4 containing specified heavy and light chain sequences, useful for
PT   treating, e.g. immune disorders.
XX
PS   Claim 3; Fig 1A; 157pp; English.
XX
CC   The present sequence represents a kappa chain of an antibody of the
CC   invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC   -4. Antibodies of the invention are composed of a heavy chain variable
CC   region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC   encoded by a human VH3-33 family gene. The modifications are contained in
CC   CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC   inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC   disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC   proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC   used to up-regulate immune system to up-regulate immunodeficient
CC   disorders
XX
SQ   Sequence 235 AA;

  Query Match             94.3%;  Score 1055.5;  DB 3;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 1.7e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||| ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||| |  :|||||||:||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS-PWTFGQGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 14
AAY93729
ID   AAY93729 standard; protein; 235 AA.
```

```
XX
AC   AAY93729;
XX
DT   03-OCT-2000  (first entry)
XX
DE   The kappa chain of immunoglobulin clone 4.1.1.
XX
KW   Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW   hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW   proliferative disorder; cancer; immunodeficient disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /note= "signal peptide"
XX
PN   WO200037504-A2.
XX
PD   29-JUN-2000.
XX
PF   23-DEC-1999;   99WO-US030895.
XX
PR   23-DEC-1998;   98US-0113647P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Hanson DC,  Neveu MJ,  Mueller EE,  Hanke JH,  Gilman SC,  Davis CG;
PI   Corvalan JR;
XX
DR   WPI; 2000-442647/38.
DR   N-PSDB; AAA46893.
XX
PT   Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT   -4 containing specified heavy and light chain sequences, useful for
PT   treating, e.g. immune disorders.
XX
PS   Claim 3; Fig 22g; 157pp; English.
XX
CC   The present sequence represents a kappa chain of an antibody of the
CC   invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC   -4. Antibodies of the invention are composed of a heavy chain variable
CC   region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC   encoded by a human VH3-33 family gene. The modifications are contained in
CC   CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC   inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC   disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC   proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC   used to up-regulate immune system to up-regulate immunodeficient
CC   disorders
XX
SQ   Sequence 235 AA;

  Query Match             94.3%;  Score 1055.5;  DB 3;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 1.7e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||| ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||| |  :|||||||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS-PWTFGQGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

```
RESULT 15
AAE35884
ID   AAE35884 standard; protein; 235 AA.
XX
AC   AAE35884;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Human 4.1.1 anti-CTLA-4 antibody kappa chain.
XX
KW   Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Signal_peptide
FT   Protein         21. .235
FT                   /note= "Mature anti-CTLA-4 antibody kappa chain"
XX
PN   EP1262193-A1.
XX
PD   04-DEC-2002.
XX
PF   23-MAY-2002; 2002EP-00253652.
XX
PR   23-MAY-2001; 2001US-0293042P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Hanson DC,  Mueller EE;
XX
DR   WPI; 2003-131215/13.
DR   N-PSDB; AAD54344.
XX
PT   Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
PT   preparation of medicament for the treatment of cancer.
XX
PS   Disclosure; Fig 1G; 76pp; English.
XX
CC   The invention relates to the use of human anti-cytotoxic T lymphocyte
CC   antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC   the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC   cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC   cancer, cancer of the anal region, stomach cancer, breast cancer,
CC   testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC   The present sequence is human anti-CTLA-4 antibody kappa chain
XX
SQ   Sequence 235 AA;

  Query Match             94.3%;  Score 1055.5;  DB 6;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 1.7e-58;
  Matches  205;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||||||||||||||||||||||||||||| ||:||||||:||| ||||||| ||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||||||:|||||||||||||| |  :|||||||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS-PWTFGQGTKVEIKRTVAAPSVFIF 139

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
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Search completed: September 8, 2005, 00:43:00
Job time : 59.1977 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:34:28 ; Search time 11.7374 Seconds
(without alignments)
1770.656 Million cell updates/sec

Title: US-10-684-957-33
Perfect score: 1119
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1017.5	90.9	215	2	JE0242	Ig kappa chain NIG
2	973.5	87.0	215	2	A23746	Ig kappa chain V-I
3	968.5	86.6	215	2	JE0244	Ig kappa chain NIG
4	932.5	83.3	215	2	JE0243	Ig kappa chain NIG
5	869	77.7	216	2	JE0241	Ig kappa chain Am3
6	734	65.6	240	2	S06084	Ig kappa chain pre
7	708	63.3	220	2	A31790	Ig kappa chain V r
8	705.5	63.0	225	2	S37484	Ig kappa chain - m
9	703.5	62.9	219	2	S38865	Ig kappa chain - m
10	702.5	62.8	219	2	S52028	Ig kappa chain - m
11	701.5	62.7	219	2	PC4203	Ig kappa chain (mo
12	696.5	62.2	217	2	S42772	Ig kappa chain - m
13	696.5	62.2	219	2	S16112	Ig kappa chain V r
14	688	61.5	214	2	S68212	Ig kappa chain (Ma
15	688	61.5	218	2	S68241	Ig kappa chain V r
16	684.5	61.2	225	2	JL0029	Ig kappa chain pre
17	682	60.9	218	2	JC5810	monoclonal antibod
18	670	59.9	234	2	S14237	Ig kappa chain pre
19	667.5	59.7	235	2	S25058	Ig kappa chain - m
20	662	59.2	234	2	S01320	Ig kappa chain pre
21	659	58.9	230	2	S33161	Ig kappa chain - s
22	654	58.4	210	2	A56169	Ig kappa chain V r
23	606.5	54.2	135	2	S52059	JC-kappa protein -
24	606.5	54.2	178	2	PT0219	Ig kappa chain V-C
25	555.5	49.6	229	2	A20969	Ig kappa chain pre
26	549.5	49.1	197	2	S29593	Ig kappa chain (WM
27	549.5	49.1	238	2	A49633	Ig lambda-like cha
28	548	49.0	106	1	K3HU	Ig kappa chain C r
29	543.5	48.6	145	2	S20631	Ig kappa chain - h
30	532	47.5	144	2	PL0106	Ig kappa chain pre
31	530	47.4	114	2	S46375	Ig kappa chain V-J
32	522.5	46.7	109	2	H30601	Ig kappa chain V-I
33	513	45.8	99	2	A37927	Ig kappa chain C r
34	512.5	45.8	108	2	C30608	Ig kappa chain V-I
35	512.5	45.8	109	2	G30601	Ig kappa chain V-I
36	512.5	45.8	109	2	B30601	Ig kappa chain V-I
37	512.5	45.8	109	2	F30607	Ig kappa chain V-I
38	512	45.8	110	2	E30607	Ig kappa chain V-I
39	511.5	45.7	107	2	PH0965	Ig kappa chain V r
40	511.5	45.7	129	2	S49532	anti-Sm antibody V
41	510.5	45.6	109	2	D30601	Ig kappa chain V-I
42	509.5	45.5	109	2	C30601	Ig kappa chain V-I
43	509.5	45.5	129	1	K3HUHA	Ig kappa chain pre
44	509.5	45.5	129	2	S46369	IG light chain var
45	509.5	45.5	134	2	S38643	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mu
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 90.9%; Score 1017.5; DB 2; Length 215;
Best Local Similarity 91.7%; Pred. No. 3.9e-62;
Matches 198; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||||||||||||||||||||: ::|||||||||| | ||||  ||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              |||||||||||| |||: |||||||||||||     :|||||||:|||||||||||||
Db         61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRP-PWTFGQGTKVEIKRTVAAPSVFIF 119

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              ||||||||||||||||||||||||||||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 2
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 973.5; DB 2; Length 215;
Best Local Similarity 91.2%; Pred. No. 3.7e-59;
Matches 196; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              ||||||||  ||||||||||||  ||||: |:|||||||||| ||||||  ||||||||
Db          1 EIVLTQSPATLSLSPGERATLSGGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||||||||:|||||||||| ||||:| : ||| |||:||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPL-TFGGGTKVEIKRTVAAPSVFIF 119

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215
              ||||||||||||||| ||||||||||||||||||
Db        180 LTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214
```

RESULT 3
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 968.5; DB 2; Length 215;
Best Local Similarity 88.0%; Pred. No. 8e-59;
Matches 190; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |:|||||| |||:|||||||||||||||: |: |||||||||| ||||||  |:||||||
Db          1 EVVLTQSPATLSVSPGERATLSCRASQSVHSN-LAWYQQKPGQAPRLLIYRASTRATGIP 59

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIF 120
              ||||||||||  |||: |: ||||:||||||      ||| |||:|||||||||||||||
Db         60 ARFSGSGSGTDFILTISSLQSEDFALYYCQQYNTWPPLTFGGGTKVEIKRTVAAPSVFIF 119

Qy        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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RESULT 4
JE0243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 932.5; DB 2; Length 215;
Best Local Similarity 84.3%; Pred. No. 2.2e-56;
Matches 183; Conservative 16; Mismatches 15; Indels 3; Gaps 3;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIP 60
              |||:|||| |||:|||||||||||||||: :: : || || || ||||||  |:||||:|
Db          1 EIVMTQSPATLSVSPGERATLSCRASQSVATN-VVWYMQKLGQAPRLLIYDASTRATGVP 59

Qy         61 DRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIK-RTVAAPSVFI 119
              |||||||||:|||||: |: ||||:||| |: |::  |||||||:| | ||||||||||
Db         60 ARFSGSGSGTEFTLTISSLQSEDFAIYYC-QHNNAWPPTFGQGTKVETKRRTVAAPSVFI 118

Qy        120 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 178

Qy        180 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||||||||||||||||||||||||||||||||||
Db        179 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match 77.7%; Score 869; DB 2; Length 216;
Best Local Similarity 79.0%; Pred. No. 4.3e-52;
Matches 173; Conservative 20; Mismatches 20; Indels 6; Gaps 4;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSII---SSYLAWYQQKPGQTPRLLIYGVSSRAT 57
              :|||||||  |::| |||||::|::|||::    ::|||||||| |:|||:  : | :
Db          1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ-PKLLIW-ANVRES 58

Qy         58 GIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSV 117
              |:|||| ||| |||||||: |: |  ||||||||  |  |:|||| :|||||||||||
Db         59 GVPDRFRGSGVGTDFTLTISNLQAELVAVYYCQQY-YSTPYSFGQGGRLEIKRTVAAPSV 117

Qy        118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 177

Qy        178 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||   |||||||||||||||||||||||||||||||||
Db        178 SSTTLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
```

RESULT 6
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084

A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 65.6%; Score 734; DB 2; Length 240;
Best Local Similarity 62.4%; Pred. No. 6.5e-43;
Matches 138; Conservative 34; Mismatches 43; Indels 6; Gaps 2;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS-----YLAWYQQKPGQTPRLLIYGVSSR 55
              : |:|||| :|::| ||  |::|::|||:  |     ||||||||||:|:||||  |:|
Db         21 DFVMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTR 80

Qy         56 ATGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAP 115
               :|:|||| ||||||||||||: :: || |:||| ||  :  |||| |||||:||  |||
Db         81 QSGVPDRFIGSGSGTDFTLTISSVQAEDLAIYYCLQYYET-PYTFGAGTKLELKRADAAP 139

Qy        116 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 175
              :| ||||| ||| :| |||||:||||||:  |:||:|  :     :|||:||||||||
Db        140 TVSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTY 199

Qy        176 SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |:||||:|||||| | :| ||| |:  |||| ||||| ||
Db        200 SMSSTLSLSKADYESHNLYTCEVVHKTSSSPVVKSFNRNEC 240
```

RESULT 7
A31790
Ig kappa chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 708; DB 2; Length 220;
Best Local Similarity 59.9%; Pred. No. 3.4e-41;
Matches 133; Conservative 36; Mismatches 45; Indels 8; Gaps 3;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS-----YLAWYQQKPGQTPRLLIYGVSSR 55
              :||:|||| :|::: ||: |:|| :|||: :|     || |||||||| |::|||  |:|
Db          1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTR 60

Qy         56 ATGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQ-QYGNSFMYTFGQGTKLEIKRTVAA 114
               :|:||||:||||||||||||: :: || ||||||  | |    ||| |||||:||  ||
Db         61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPL--TFGGGTKLELKRADAA 118

Qy        115 PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST 174
              |:| ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||
Db        119 PTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDST 178

Qy        175 YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              ||:|||||:| :||:|  | || ||:  :||: |||||  ||
Db        179 YSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 220
```

RESULT 8
S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 63.0%; Score 705.5; DB 2; Length 225;
Best Local Similarity 62.8%; Pred. No. 5.2e-41;
Matches 135; Conservative 33; Mismatches 44; Indels 3; Gaps 2;

```
Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSIISSYLAWYQQKPGQTPRLLIYGVSSRATGIPD 61
              ||:||:|  | || |:| |::|:|||| :|: :|||||||||:|:||||  ||| ||:||
Db         14 IVMTQTPKFLLLSAGDRVTITCKASQS-VSNDVAWYQQKPGQSPKLLIYYASSRYTGVPD 72

Qy         62 RFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVFIFP 121
              ||:||| ||||| ||: :: || |||:|||  :|  |||| ||||||||  |||:| |||
Db         73 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSS--YTFGGGTKLEIKRADAAPTVSIFP 130

Qy        122 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 181
              || ||| || ||||| |||||::  |:||:| : :      | |:|||||||:||||
Db        131 PSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTL 190

Qy        182 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              ||:| :||:|  | || ||:  :||: ||||| ||
Db        191 TLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 225
```

RESULT 9
S38865
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of a
A;Reference number: S38864
A;Accession: S38865
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <KIP>
A;Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 62.9%; Score 703.5; DB 2; Length 219;
Best Local Similarity 60.9%; Pred. No. 6.9e-41;
Matches 134; Conservative 37; Mismatches 44; Indels 5; Gaps 2;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSII----SSYLAWYQQKPGQTPRLLIYGVSSRA 56
              |:|:|||| :|||:| |::|::||:|||::    ::|| || |||| :|:|||| ||:|
Db          1 ELVMTQSPLSLSVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGLSPKLLIYIVSNRF 60

Qy         57 TGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPS 116
              :|:|||||||||||||| |:|:| ||  ||:|  |       :||| ||||||||  |||:
Db         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQV-THVPWTFGGGTKLEIKRADAAPT 119

Qy        117 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 176
              | ||||| ||| || ||||| |||||::  |:||:| : :      | |:|||||||
Db        120 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 179

Qy        177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              :||||||:| :||:|  | || ||:  :||: ||||||||
Db        180 MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 219
```

```
RESULT 10
S52028
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun
A;Reference number: S52028
A;Accession: S52028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

  Query Match             62.8%;  Score 702.5;  DB 2;  Length 219;
  Best Local Similarity   61.4%;  Pred. No. 8.1e-41;
  Matches  135;  Conservative   34;  Mismatches   46;  Indels    5;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS----YLAWYQQKPGQTPRLLIYGVSSRA 56
              ::|:|||| :| :| |::|::|||:|||: |    || || |||||:|:|||| ||:|
Db          1 DVVMTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60

Qy         57 TGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPS 116
              :|:|||||||||||||| |:|:| ||  |||| | |:    ||| || |||||  |||:
Db         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQ-GSHVPPTFGGGTNLEIKRADAAPT 119

Qy        117 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 176
              | ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||||
Db        120 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 179

Qy        177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              :||||||:| :||:|  | || ||:  :||: ||||| ||
Db        180 MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219


RESULT 11
PC4203
Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mo
A;Reference number: PC4202; MUID:97082978; PMID:8964510
A;Accession: PC4203
A;Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

  Query Match             62.7%;  Score 701.5;  DB 2;  Length 219;
  Best Local Similarity   60.5%;  Pred. No. 9.4e-41;
  Matches  133;  Conservative   38;  Mismatches   44;  Indels    5;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSII----SSYLAWYQQKPGQTPRLLIYGVSSRA 56
              ::::||:| :| :| |::|::|||:||||:    ::|| || |||||:|:|||| ||:|
Db          1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHTNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60

Qy         57 TGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPS 116
              :|:|||||||||||||| |:|:| ||  |||| | |:    ||| ||||||||  |||:
Db         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQ-GSHVPRTFGGGTKLEIKRADAAPT 119

Qy        117 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 176
              | ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||||
Db        120 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 179

Qy        177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              :||||||:| :||:|  | || ||:  :||: ||||| ||
Db        180 MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219


RESULT 12
S42772
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42772
R;Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42771
A;Accession: S42772
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <SCH>
A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-93/Domain: immunoglobulin homology <IMM>

  Query Match             62.2%;  Score 696.5;  DB 2;  Length 217;
  Best Local Similarity   60.1%;  Pred. No. 2e-40;
  Matches  131;  Conservative   37;  Mismatches   45;  Indels    5;  Gaps    2;

Qy          3 VLTQSPGTLSLSPGERATLSCRASQSII----SSYLAWYQQKPGQTPRLLIYGVSSRATG 58
              |:|||| :| :| |::|::|||:|||::    ::|| || |||||:|::||| ||:| :|
Db          1 VMTQSPLSLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGQSPKVLIYKVSTRFSG 60

Qy         59 IPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSVF 118
              :|||||||||||||  |:|:| ||  ||:| |       :||| |||||||  |||:|
Db         61 VPDRFSGSGSGTDFTFKISRVEAEDLGVYFCSQ-STYVPFTFGSGTKLEIKRADAAPTVS 119

Qy        119 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 178
              ||||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||:|
Db        120 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 179

Qy        179 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
              |||||:| :||:|  | || ||:  :||: ||||||||
Db        180 STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 217


RESULT 13
S16112
Ig kappa chain V region (G2a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16112
R;Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.;
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(
A;Reference number: S16112; MUID:92000313; PMID:1910583
A;Accession: S16112
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-219 <BIT>
A;Cross-references: UNIPROT:Q8VCI6; UNIPROT:Q99M37
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

  Query Match             62.2%;  Score 696.5;  DB 2;  Length 219;
  Best Local Similarity   60.0%;  Pred. No. 2.1e-40;
  Matches  132;  Conservative   37;  Mismatches   46;  Indels    5;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS----YLAWYQQKPGQTPRLLIYGVSSRA 56
              ::|:||:| :| :| |::|::|||:|||:: |    || || |||||:|: ||| ||:|
Db          1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRF 60
```

```
Qy          57 TGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPS 116
               :|:|||||||||||||||| |:|:| ||  ||:| | |    |||| ||:|||||  |||:
Db          61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFQ-GTHVPYTFGGGTRLEIKRADAAPT 119

Qy         117 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 176
               | ||||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||
Db         120 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 179

Qy         177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
               :|||||:| :||:|  | || ||:  :||: ||||| ||
Db         180 MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219


RESULT 14
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68212
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68212
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-214 <TAK>
A;Cross-references: EMBL:D29668
C;Superfamily: immunoglobulin V region; immunoglobulin homology

  Query Match           61.5%;  Score 688;  DB 2;  Length 214;
  Best Local Similarity  60.0%;  Pred. No. 7.6e-40;
  Matches  129;  Conservative   39;  Mismatches   41;  Indels    6;  Gaps    2;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS-----YLAWYQQKPGQTPRLLIYGVSSR 55
               :||:|||| :|::| |:: |:|||::|||:::|     ||||||||||:|:||:|  |:|
Db           1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQSPKLLVYFASTR 60

Qy          56 ATGIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAP 115
                :|:|||| |||||||||||: :: || | |:|||:  |  |||| ||||||||  |||
Db          61 ESGVPDRFIGSGSGTDFTLTISTVQAEDLADYFCQQH-YSTPYTFGGGTKLEIKRADAAP 119

Qy         116 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 175
               :| ||||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||
Db         120 TVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTY 179

Qy         176 SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS 210
               |:||||||:| :||:|  | || ||:  :||: ||
Db         180 SMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS 214


RESULT 15
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyri
A;Reference number: S68241
A;Accession: S68241
A;Molecule type: mRNA
A;Residues: 1-218 <TAK>
A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68214
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'NI',3-212 <TAW>
A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

  Query Match           61.5%;  Score 688;  DB 2;  Length 218;
  Best Local Similarity  60.3%;  Pred. No. 7.7e-40;
  Matches  132;  Conservative   33;  Mismatches   50;  Indels    4;  Gaps    2;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSIISS---YLAWYQQKPGQTPRLLIYGVSSRAT 57
               |:|||||| :|::| |:|||:|||||:|: :|   |: |||||||| |:|||   ::  :
Db           1 ELVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLATNLES 60

Qy          58 GIPDRFSGSGSGTDFTLTITRLEPEDFAVYYCQQYGNSFMYTFGQGTKLEIKRTVAAPSV 117
               |:| |||||||||||||| |  :| || | ||| |:      ||| |||||:||  |||:|
Db          61 GVPARFSGSGSGTDFTLNIHPVEEEDVATYYC-QHSRELPLTFGAGTKLELKRADAAPTV 119

Qy         118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 177
                ||||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||:
Db         120 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 179

Qy         178 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
               ||||||:| :||:|  | || ||:  :||: ||||||||
Db         180 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 218


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Job time : 12.7374 secs
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:14:16 ; Search time 111.328 Seconds
(without alignments)
1581.260 Million cell updates/sec

Title: US-10-684-957-32
Perfect score: 2394
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2394	100.0	447	17	US-10-684-957-32	Sequence 32, Appl
2	2386	99.7	447	17	US-10-684-957-19	Sequence 19, Appl
3	2383	99.5	447	17	US-10-684-957-21	Sequence 21, Appl
4	2360	98.6	447	17	US-10-684-957-17	Sequence 17, Appl
5	2296.5	95.9	468	16	US-10-769-144-2	Sequence 2, Appli
6	2296.5	95.9	468	18	US-10-903-191-2	Sequence 2, Appli
7	2296.5	95.9	613	16	US-10-769-144-10	Sequence 10, Appl
8	2296.5	95.9	613	18	US-10-903-191-10	Sequence 10, Appl
9	2274	95.0	474	15	US-10-291-265-284	Sequence 284, App
10	2259.5	94.4	467	15	US-10-656-769-32	Sequence 32, Appl
11	2228	93.1	451	17	US-10-849-615-69	Sequence 69, Appl
12	2174	90.8	470	14	US-10-216-484-157	Sequence 157, App
13	2174	90.8	470	14	US-10-384-933-157	Sequence 157, App
14	2170	90.6	470	14	US-10-216-484-147	Sequence 147, App
15	2170	90.6	470	14	US-10-384-933-147	Sequence 147, App
16	2169	90.6	470	14	US-10-216-484-145	Sequence 145, App
17	2169	90.6	470	14	US-10-384-933-145	Sequence 145, App
18	2167	90.5	470	14	US-10-216-484-143	Sequence 143, App
19	2167	90.5	470	14	US-10-384-933-143	Sequence 143, App
20	2166	90.5	470	14	US-10-216-484-117	Sequence 117, App
21	2166	90.5	470	14	US-10-384-933-117	Sequence 117, App
22	2164.5	90.4	452	16	US-10-818-765-4	Sequence 4, Appli
23	2164.5	90.4	452	17	US-10-861-049-16	Sequence 16, Appl
24	2164.5	90.4	452	20	US-11-021-874-16	Sequence 16, Appl
25	2164.5	90.4	452	20	US-11-005-677-4	Sequence 4, Appli
26	2164.5	90.4	471	17	US-10-877-363-4	Sequence 4, Appli
27	2164.5	90.4	471	17	US-10-922-651-4	Sequence 4, Appli
28	2164.5	90.4	471	17	US-10-861-049-4	Sequence 4, Appli
29	2164.5	90.4	471	20	US-11-021-874-4	Sequence 4, Appli
30	2160	90.2	448	15	US-10-411-037-56	Sequence 56, Appl
31	2160	90.2	448	15	US-10-411-026-56	Sequence 56, Appl
32	2160	90.2	448	15	US-10-410-962-56	Sequence 56, Appl
33	2160	90.2	448	15	US-10-411-049-56	Sequence 56, Appl
34	2160	90.2	448	16	US-10-410-930-56	Sequence 56, Appl
35	2160	90.2	448	16	US-10-410-997-56	Sequence 56, Appl
36	2160	90.2	448	16	US-10-411-012-56	Sequence 56, Appl
37	2160	90.2	448	16	US-10-287-994-56	Sequence 56, Appl
38	2160	90.2	448	16	US-10-410-913-56	Sequence 56, Appl
39	2160	90.2	448	17	US-10-410-980-56	Sequence 56, Appl
40	2160	90.2	448	17	US-10-410-897-56	Sequence 56, Appl
41	2160	90.2	448	17	US-10-492-261-56	Sequence 56, Appl
42	2158.5	90.2	731	9	US-09-825-012-46	Sequence 46, Appl
43	2158.5	90.2	741	9	US-09-825-012-55	Sequence 55, Appl
44	2158	90.1	470	14	US-10-216-484-89	Sequence 89, Appl
45	2158	90.1	470	14	US-10-384-933-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-10-684-957-32
; Sequence 32, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-32

Query Match 100.0%; Score 2394; DB 17; Length 447;
Best Local Similarity 100.0%; Pred. No. 4.2e-151;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
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Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

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Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120

Qy         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 2
US-10-684-957-19
; Sequence 19, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-19

Query Match 99.7%; Score 2386; DB 17; Length 447;
Best Local Similarity 99.8%; Pred. No. 1.4e-150;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
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Db           1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
               |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 3
US-10-684-957-21
; Sequence 21, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-21

Query Match 99.5%; Score 2383; DB 17; Length 447;
Best Local Similarity 99.6%; Pred. No. 2.3e-150;
Matches 445; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
               ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
               |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
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Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 4
US-10-684-957-17
; Sequence 17, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 447
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-684-957-17

Query Match 98.6%; Score 2360; DB 17; Length 447;
Best Local Similarity 99.1%; Pred. No. 7.7e-149;
Matches 443; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||||:|||||||||||||||||| ||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||||:|||| ||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 5
US-10-769-144-2
; Sequence 2, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-2

Query Match 95.9%; Score 2296.5; DB 16; Length 468;
Best Local Similarity 96.2%; Pred. No. 1.4e-144;
Matches 434; Conservative 3; Mismatches 5; Indels 9; Gaps 2;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||:||||||| |||:||||||||||||||||||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG----SYWYFDLRGRGTLVTVS 116
              |||||||||||||||||||||||||||||||||||| |    ||     |:|||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDRGVDYW-----GQGTLVTVS 134

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 194

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 254

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 314

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 374

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 434

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        435 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465
```

RESULT 6
US-10-903-191-2
; Sequence 2, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky

```
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301CP
;  CURRENT APPLICATION NUMBER: US/10/903,191
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 10/769144
;  PRIOR FILING DATE: 2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 468
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-903-191-2

  Query Match             95.9%;  Score 2296.5;  DB 18;  Length 468;
  Best Local Similarity   96.2%;  Pred. No. 1.4e-144;
  Matches  434;  Conservative    3;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||| |||:||||||||||||||||||||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG----SYWYFDLRGRGTLVTVS 116
              |||||||||||||||||||||||||||||||  |    ||     |:|||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDRGVDYW-----GQGTLVTVS 134

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 194

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 254

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 314

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 374

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 434

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        435 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 7
US-10-769-144-10
; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Endres, Michael
;  APPLICANT:  He, Lizhen
;  APPLICANT:  Ramakrishna, Venky
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301
;  CURRENT APPLICATION NUMBER: US/10/769,144
;  CURRENT FILING DATE:  2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-769-144-10

  Query Match             95.9%;  Score 2296.5;  DB 16;  Length 613;
  Best Local Similarity   96.2%;  Pred. No. 1.8e-144;
  Matches  434;  Conservative    3;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||| |||:||||||||||||||||||||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG----SYWYFDLRGRGTLVTVS 116
              |||||||||||||||||||||||||||||||  |    ||     |:|||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDRGVDYW-----GQGTLVTVS 134

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 194

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 254

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 314

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 374

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 434

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        435 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 8
US-10-903-191-10
; Sequence 10, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Endres, Michael
;  APPLICANT:  He, Lizhen
;  APPLICANT:  Ramakrishna, Venky
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301CP
;  CURRENT APPLICATION NUMBER: US/10/903,191
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 10/769144
;  PRIOR FILING DATE: 2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-903-191-10

  Query Match             95.9%;  Score 2296.5;  DB 18;  Length 613;
  Best Local Similarity   96.2%;  Pred. No. 1.8e-144;
  Matches  434;  Conservative    3;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
```

```
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG----SYWYFDLRGRGTLVTVS 116
              ||||||||||||||||||||||||||||||||||||  |    ||     |:|||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDRGVDYW-----GQGTLVTVS 134

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 194

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 254

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 314

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 374

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 434

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        435 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465
```

RESULT 9
US-10-291-265-284
; Sequence 284, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 284
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-284

Query Match 95.0%; Score 2274; DB 15; Length 474;
Best Local Similarity 94.1%; Pred. No. 4.3e-143;
Matches 428; Conservative 8; Mismatches 11; Indels 8; Gaps 2;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||||||: ||: |||| | ||| ||||||||||||||
Db         20 EVQLVQSGAEVKKPGESVKISCKGSGYSFSDYWVAWVRQSPDKGLAWMGIIYPGDSDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG------SYWYF--DLRGRGTL 112
              |||||||||||||||||||||||||| |||||||  |      || |:  |: ||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKDSDTAMYYCARGARGTAPSYHYYGLDVWGRGTS 139

Qy        113 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199

Qy        173 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 232
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        200 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259

Qy        233 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 319

Qy        293 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 379

Qy        353 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 412
              |||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 439

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||||
Db        440 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
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RESULT 10
US-10-656-769-32
; Sequence 32, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-32

Query Match 94.4%; Score 2259.5; DB 15; Length 467;
Best Local Similarity 95.1%; Pred. No. 3.9e-142;
Matches 426; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||:|||||||||||||||||||||: :|| ||||||||||||||:|| |||||
Db         20 EVQLMQSGAEVKKPGESLKISCKGSGYSFSFHWIAWVRQMPGKGLEWMGIIHPGASDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYWYFDLRGRGTLVTVSSAS 119
              |||||||||||| | |  ||||||||||||||:|       |||  |:||||||||||
Db         80 SPSFQGQVTISADNSNSATYLQWSSLKASDTAMYFCARQRELDYFDYWGQGTLVTVSSAS 139

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 199

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 259

Qy        240 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 319

Qy        300 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 379
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Qy        360 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 439

Qy        420 GNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||
Db        440 GNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 11
US-10-849-615-69
; Sequence 69, Application US/10849615
; Publication No. US20050025764A1
; GENERAL INFORMATION:
;  APPLICANT: Allan, Barrett W.
;  APPLICANT:  Davies, Julian
;  APPLICANT:  Marquis, David M.
;  APPLICANT:  Ondek, Brian
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: CD20 BINDING MOLECULES
;  FILE REFERENCE: AME-09016
;  CURRENT APPLICATION NUMBER: US/10/849,615
;  CURRENT FILING DATE:  2004-05-20
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(451)
;   OTHER INFORMATION: AME 33 complete heavy chain
US-10-849-615-69

  Query Match             93.1%;  Score 2228;  DB 17;  Length 451;
  Best Local Similarity   93.6%;  Pred. No. 4.7e-140;
  Matches  422;  Conservative    7;  Mismatches   18;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||||||||| :|||| : ||||||||||||||| |||   || |
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTGDTSY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY----WYFDLRGRGTLVTVS 116
              :   : |||||||||||||||||||||||||||||    :|     | ||: |:|| ||||
Db         61 NQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDWQFDVWGKGTTVTVS 120

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 240

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        421 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 12
US-10-216-484-157
; Sequence 157, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976A1ufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 157
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed
;   OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-216-484-157

  Query Match             90.8%;  Score 2174;  DB 14;  Length 470;
  Best Local Similarity   89.8%;  Pred. No. 1.9e-136;
  Matches  405;  Conservative   20;  Mismatches   22;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|||||: |||| ||:|||||| | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYWYFDLRGRGTLVTVS 116
              :  |:|:|||: | | ||||:: |||:: |||:|||      : ||||: | |||||||
Db         80 NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 13
US-10-384-933-157
; Sequence 157, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030170817A1ufusa
;  APPLICANT:  Haruyama, Hideyuki
```

; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 157
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed
; OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-384-933-157

Query Match 90.8%; Score 2174; DB 14; Length 470;
Best Local Similarity 89.8%; Pred. No. 1.9e-136;
Matches 405; Conservative 20; Mismatches 22; Indels 4; Gaps 1;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|||||: |||| ||:|||||| | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYWYFDLRGRGTLVTVS 116
              :  |:|:|||: | | ||||:: |||:: |||:|||       : ||||: | |||||||
Db         80 NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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RESULT 14
US-10-216-484-147
; Sequence 147, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-147

Query Match 90.6%; Score 2170; DB 14; Length 470;
Best Local Similarity 89.4%; Pred. No. 3.6e-136;
Matches 403; Conservative 22; Mismatches 22; Indels 4; Gaps 1;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|||||: |||| ||:|||||| | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYWYFDLRGRGTLVTVS 116
              :  |:|: |:: | | ||||:: |||:: |||:|||       : ||||: |:|||||||
Db         80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
```

RESULT 15
US-10-384-933-147
; Sequence 147, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;   OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-147

  Query Match             90.6%;  Score 2170;  DB 14;  Length 470;
  Best Local Similarity   89.4%;  Pred. No. 3.6e-136;
  Matches  403;  Conservative   22;  Mismatches   22;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|||||: |||| ||:|||||| | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYWYFDLRGRGTLVTVS 116
              :  |:|: |:: | | ||||:: |||:: |||:|||       : ||||: |:|||||||
Db         80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              |||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


Search completed: September  8, 2005, 00:48:34
Job time : 113.328 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 00:15:52 ; Search time 108.629 Seconds
(without alignments)
2107.158 Million cell updates/sec

Title: US-10-684-957-32
Perfect score: 2394
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2121.5	88.6	469	2	Q7Z7P5	Q7z7p5 homo sapien
2	2095.5	87.5	475	2	Q6N095	Q6n095 homo sapien
3	2095	87.5	470	2	Q6PJA4	Q6pja4 homo sapien
4	2092	87.4	480	2	Q6PJF1	Q6pjf1 homo sapien
5	2090.5	87.3	475	2	Q6MZQ6	Q6mzq6 homo sapien
6	2077	86.8	478	2	Q6PI81	Q6pi81 homo sapien
7	2073	86.6	466	2	Q6N096	Q6n096 homo sapien
8	2068	86.4	466	2	Q6IN78	Q6in78 homo sapien
9	2061.5	86.1	544	2	Q6PJ95	Q6pj95 homo sapien
10	2060.5	86.1	465	2	Q6GMX6	Q6gmx6 homo sapien
11	2059	86.0	472	2	Q6N089	Q6n089 homo sapien
12	2057	85.9	480	2	Q6N094	Q6n094 homo sapien
13	2056.5	85.9	473	2	Q6P055	Q6p055 homo sapien
14	2051.5	85.7	473	2	Q6MZV7	Q6mzv7 homo sapien
15	2029	84.8	476	2	Q6GMX1	Q6gmx1 homo sapien
16	2027	84.7	470	2	Q7Z5W1	Q7z5w1 homo sapien
17	2026	84.6	482	2	Q7Z351	Q7z351 homo sapien
18	2022.5	84.5	475	2	Q6GMW7	Q6gmw7 homo sapien
19	2008.5	83.9	481	2	Q6N097	Q6n097 homo sapien
20	1985	82.9	518	2	Q6N030	Q6n030 homo sapien
21	1926.5	80.5	521	2	Q8N4Y9	Q8n4y9 homo sapien
22	1907.5	79.7	465	2	Q6P6C4	Q6p6c4 homo sapien
23	1886	78.8	464	2	Q6MZU6	Q6mzu6 homo sapien
24	1851	77.3	493	2	Q68CN4	Q68cn4 homo sapien
25	1839	76.8	473	2	Q8TC63	Q8tc63 homo sapien
26	1814	75.8	417	2	Q6N093	Q6n093 homo sapien
27	1806	75.4	348	2	Q6PYX1	Q6pyx1 homo sapien
28	1805.5	75.4	476	2	Q6MZX7	Q6mzx7 homo sapien
29	1767	73.8	330	1	GC1_HUMAN	P01857 homo sapien
30	1616.5	67.5	509	2	Q8NF17	Q8nf17 homo sapien
31	1604	67.0	326	1	GC2_HUMAN	P01859 homo sapien
32	1590.5	66.4	327	1	GC4_HUMAN	P01861 homo sapien
33	1543.5	64.5	487	2	Q65ZL2	Q65zl2 mus sp. fv/
34	1524.5	63.7	354	2	Q86TT2	Q86tt2 homo sapien
35	1522	63.6	470	2	Q7TMK1	Q7tmk1 mus musculu
36	1511.5	63.1	463	2	Q99LC4	Q99lc4 mus musculu
37	1498.5	62.6	473	2	Q9D8L4	Q9d8l4 mus musculu
38	1476	61.7	464	2	Q6PF95	Q6pf95 mus musculu
39	1472.5	61.5	465	2	Q6PJB2	Q6pjb2 mus musculu
40	1452	60.7	472	2	Q6PJA7	Q6pja7 mus musculu
41	1443	60.3	474	2	Q8R3H6	Q8r3h6 mus musculu
42	1419	59.3	458	2	Q65ZQ1	Q65zq1 homo sapien
43	1400.5	58.5	471	2	Q66K04	Q66k04 mus musculu
44	1397	58.4	464	2	Q6PIP8	Q6pip8 mus musculu
45	1372.5	57.3	473	2	Q91Z05	Q91z05 mus musculu

ALIGNMENTS

RESULT 1
Q7Z7P5
ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 88.6%; Score 2121.5; DB 2; Length 469;

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  Best Local Similarity   88.4%;  Pred. No. 8.1e-135;
  Matches  398;  Conservative   24;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :| |||||||||||| |:|:||| |||:|:|| : |||| ||:|||||| |   : ||:|
Db         20 QVHLVQSGAEVKKPGASVKLSCKTSGYNFSSYDLIWVRQAPGQGLEWMGWISAHNGDTKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS---GSYWYFDLRGRGTLVTVSS 117
              :  |||:||:: | | :|:|::: ||:: |||::|| :   |    ||  |:||||||
Db         80 ARKFQGRVTMTTDTSATTSYMEFRSLRSDDTALFYCATKSRGQVGDFDSWGQGTLVTVSS 139

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 199

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 259

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 379

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 439

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        440 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469
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```
RESULT 2
Q6N095
ID   Q6N095      PRELIMINARY;      PRT;   475 AA.
AC   Q6N095;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686K03196.
GN   Name=DKFZp686K03196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640621; CAE45775.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52360 MW;  7BA14104CD2DB8F0 CRC64;

  Query Match             87.5%;  Score 2095.5;  DB 2;  Length 475;
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  Best Local Similarity   86.2%;  Pred. No. 4.6e-133;
  Matches  393;  Conservative   25;  Mismatches   29;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||:|:|| |: |||: |||||::| | |||| ||: |||||||: |     |
Db         20 QVQLVQSGAELKRPGASVTISCRASGYSFSTYHIHWVRQAPGQRLEWMGIMNPRSDSKTY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYWY-----FDLRGRGT 111
              : :|||::|:: | | || ::: :|||: |||:|||       : |:     ||: |:||
Db         80 AQTFQGRMTMTRDTSTSTVFMELNSLKSGDTAVYYCTRDRSGRALWFGELDAFDIWGQGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWVSNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475
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RESULT 3
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
```

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match           87.5%;  Score 2095;  DB 2;  Length 470;
  Best Local Similarity   87.8%;  Pred. No. 5e-133;
  Matches  396;  Conservative   20;  Mismatches   31;  Indels    4;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::|| ||::|:|||: |||| |||||||:  |    |:  |
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYWY---FDLRGRGTLVTVS 116
                | :|: ||| | : :: ||| :||:| |||:|||   || ||   ||  |:|||||||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 4
Q6PJF1
ID   Q6PJF1      PRELIMINARY;      PRT;   480 AA.
AC   Q6PJF1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016381; AAH16381.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   480 AA;  52586 MW;  64DC641AE47CD6C8 CRC64;

  Query Match           87.4%;  Score 2092;  DB 2;  Length 480;
  Best Local Similarity   86.3%;  Pred. No. 8.1e-133;
  Matches  398;  Conservative   20;  Mismatches   29;  Indels   14;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| || |  |: | |||| ||:|| ||| | |    |:|
Db         20 QVQLVQSGAEVKKPGSSVKVSCKASGGSPGSFVISWVRQAPGQGLAWMGGIIPAFDITKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG---------SG-----SYWYFDL 106
              : :|| :|||||:|  |||::  ||:: ||| |||           ||      |:  |:
Db         80 AQNFQDRVTISADESTDTAYMELRSLRSEDTATYYCARDLALYELWSGFHTDEKYYGLDV 139

Qy        107 RGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 166
               |:|| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 WGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 199

Qy        167 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 226
              |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        200 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTC 259

Qy        227 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319

Qy        287 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 379

Qy        347 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 406
              |||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||
Db        380 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 439
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Qy        407 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||||||||||
Db        440 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 480


RESULT 5
Q6MZQ6
ID   Q6MZQ6      PRELIMINARY;      PRT;   475 AA.
AC   Q6MZQ6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686G11190.
GN   Name=DKFZp686G11190;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640947; CAE45972.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52043 MW;  B7EAE255A26F4B8E CRC64;

  Query Match             87.3%;  Score 2090.5;  DB 2;  Length 475;
  Best Local Similarity   86.2%;  Pred. No. 1e-132;
  Matches  393;  Conservative   22;  Mismatches   32;  Indels    9;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||::||  : :|| ||::||  ||::| :| : |||| |||||||:  |     :| |
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMNWVRQAPGKGLEWVSGISSSGVNTYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG---------SGSYWYFDLRGRGT 111
              : | :|: ||| | | :| |||  ||:| |||:|||         | :|||||: ||||
Db         80 ADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              ||:||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439


Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 6
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match             86.8%;  Score 2077;  DB 2;  Length 478;
  Best Local Similarity   85.0%;  Pred. No. 8.3e-132;
  Matches  390;  Conservative   26;  Mismatches   31;  Indels   12;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||::|:|||: |||| |||||||:  |     |: |
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG----------SGSYWYF--DLRG 108
              | :|: ||| | : :: ||| :||:| |||:|||           :  |:||  |: |
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139
```

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Qy        109 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 168
              :|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy        169 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 228
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP 259

Qy        229 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy        289 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy        349 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 408
              |||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439

Qy        409 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||||||||
Db        440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 7
Q6N096
ID Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I15196.
GN Name=DKFZp686I15196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX640620; CAE45774.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 86.6%; Score 2073; DB 2; Length 466;
Best Local Similarity 87.0%; Pred. No. 1.5e-131;
Matches 389; Conservative 22; Mismatches 36; Indels 0; Gaps 0;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||:||  : :|| |||:||  ||::  :||:  ||| ||||| |: ::    |:| |
Db         20 EVQLVESGGGLVQPGGSLKLSCAASGFTVNNYWMHRVRQAPGKGLVWVSLMRDDASETAY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              :   ||: ||| | : :| :|| |||:| |||:|||  | :  ||  |:||||||||||
Db         80 AEFVQGRFTISRDNAKNTLFLQLSSLRAEDTAVYYCARGGFGNFDQWGQGTLVTVSSAST 139
```

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Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 199

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 259

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 319

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        320 RVVSVLTVLHQDWLNGKEYKCRVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 379

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 439

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||| ||||||||||||||||
Db        440 NVFSCSVMHEGLHNHYTQKSLSLSPGK 466
```

RESULT 8
Q6IN78
ID Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

```
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   466 AA;  50853 MW;  53EB0BCEDE81076E CRC64;

  Query Match             86.4%;  Score 2068;  DB 2;  Length 466;
  Best Local Similarity   86.5%;  Pred. No. 3.2e-131;
  Matches  392;  Conservative   22;  Mismatches   27;  Indels   12;  Gaps    3;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||:||  : :|| || :||  || : :| :: |||| |||||||: ::| | : | |
Db         20 EVQLVESGGGLIQPGGSLTLSCAASGLTVSSNYMHWVRQAPGKGLEWVSVLYIGGA-TYY 78

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY------WYFDLRGRGTLVT 114
              : | :|: ||| | | :| ||| :||:| |||:||| |:|      |     |:|||||
Db         79 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGNYVVPAAPW-----GQGTLVT 133

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 193

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        194 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEL 253

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 313

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 373

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 433

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        434 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 9
Q6PJ95
ID   Q6PJ95      PRELIMINARY;      PRT;   544 AA.
AC   Q6PJ95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019046; AAH19046.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   544 AA;  60102 MW;  1895814B2297C668 CRC64;

  Query Match             86.1%;  Score 2061.5;  DB 2;  Length 544;
  Best Local Similarity   85.9%;  Pred. No. 1.1e-130;
  Matches  390;  Conservative   19;  Mismatches   36;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              : |||:||  | :|| ||::||  ||: |::| : |||| |||||||: :    :||  |
Db         20 QAQLVESGGGVVQPGSSLRLSCAASGFRFSNYGMHWVRQAPGKGLEWVAVFSYDESDKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-WY--------FDLRGRGT 111
              : | :|: ||| | | :|  || :||:  |||:|||       ||         ||  ||||
Db         80 AASVKGRFTISRDNSKNTLSLQMNSLRVEDTAVYYCAKDQKPWYSNSWFLTNFDSWGRGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 445
              |||||||||||||||||||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 473


RESULT 10
Q6GMX6
ID   Q6GMX6      PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;

  Query Match           86.1%;  Score 2060.5;  DB 2;  Length 465;
  Best Local Similarity  87.0%;  Pred. No. 1e-130;
  Matches  389;  Conservative   21;  Mismatches   36;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :||| :||  : || |:| ::|  || | : |:  |:||  ||||||:| ||   | | |
Db         20 QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPAGKGLEWIGRIYTSGS-TNY 78

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              :|| : :||:| | | :   |: ||: |:|||:|||  | : |||  |:||||||||||
Db         79 NPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGRFTYFDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 11
Q6N089
ID   Q6N089      PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match           86.0%;  Score 2059;  DB 2;  Length 472;
  Best Local Similarity  85.7%;  Pred. No. 1.3e-130;
  Matches  388;  Conservative   25;  Mismatches   34;  Indels    6;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||::|  | : |||| |||||||:  |         |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYWYF--DLRGRGTLVT 114
              : | :|: ||| |   :: ||| :||:| |||:|||    |: :::|:  |: |:|| ||
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAKEIGAHNFYYYGMDVWGQGTTVT 139

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 199

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        200 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEL 259

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 319

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 379

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 439

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
                ||||||||||||||||||||||||||||||||
Db        440 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 12
Q6N094
ID   Q6N094      PRELIMINARY;      PRT;   480 AA.
AC   Q6N094;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686O01196.
GN   Name=DKFZp686O01196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640622; CAE45776.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   480 AA;  52612 MW;  225247F3D35AEC18 CRC64;

  Query Match             85.9%;  Score 2057;  DB 2;  Length 480;
  Best Local Similarity   84.0%;  Pred. No. 1.9e-130;
  Matches  388;  Conservative   23;  Mismatches   35;  Indels   16;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              | :||:||  : ||||||::||  ||::| |: : |||| |||||||:  |    ::  |
Db         20 EEELVESGGGLVKPGESLRLSCAASGFTFRSFNMNWVRQAPGKGLEWIAFINSRGNEKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYW---------------YFD 105
                | :|: ||| | : :: :|| |||:  |||:|||  |  |               :||
Db         80 GESVKGRFTISRDNADNSLFLQMSSLRVDDTAIYYCARGK-WVPAGPTSTSGPVRHNWFD 138

Qy        106 LRGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 165
              |:||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PWGQGTLVTISSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 198

Qy        166 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 225
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 258

Qy        226 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 285
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 318

Qy        286 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 345
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 378

Qy        346 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 405
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 438

Qy        406 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
                |||||||||||||||||||||||| ||||||||||||||||
Db        439 LYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 480


RESULT 13
Q6P055
ID   Q6P055      PRELIMINARY;      PRT;   473 AA.
AC   Q6P055;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC065820; AAH65820.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51344 MW;  9816D56A77129B57 CRC64;
```

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  Query Match           85.9%;  Score 2056.5;  DB 2;  Length 473;
  Best Local Similarity  85.7%;  Pred. No. 2e-130;
  Matches  389;  Conservative   18;  Mismatches   40;  Indels    7;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGD--SDT 58
              |  ||:||  : :|| || :|| |||::|:  |: |||| |||||||:  |    |    |
Db         20 EAHLVESGGGLVRPGGSLTLSCTGSGFTFSGAWLSWVRQAPGKGLEWVARIQTEDDGGTT 79

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS-----YWYFDLRGRGTLV 113
               |  : :|: |:| | | :| ||| | |:  ||| |:| :||         ||  |:|||
Db         80 HYGIAVKGRFTVSRDDSRNTLYLQMSDLRTEDTAFYFCATGSMNTVGLTGFDSWGQGTLV 139

Qy        114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 199

Qy        174 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 259

Qy        234 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        294 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        354 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        414 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||| ||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 473
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RESULT 14
Q6MZV7
ID   Q6MZV7      PRELIMINARY;      PRT;   473 AA.
AC   Q6MZV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   Name=DKFZp686C11235;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RG   The German Human cDNA Consortium;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;
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  Query Match           85.7%;  Score 2051.5;  DB 2;  Length 473;
  Best Local Similarity  85.2%;  Pred. No. 4.3e-130;
  Matches  387;  Conservative   25;  Mismatches   35;  Indels    7;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |:|||:||  : :|| ||::||  ||::|:|: : |||| |||||||:  |    :  |
Db         20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG----SGSYWY---FDLRGRGTLV 113
              : | ||: ||| | : :: ||| :||:| |||:|||       | ||   ||  |:| ||
Db         80 ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV 139

Qy        114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSWNSGALTSGVHTFPAV 199

Qy        174 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 233
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 259

Qy        234 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        294 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        354 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 413
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        414 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 15
Q6GMX1
ID   Q6GMX1      PRELIMINARY;      PRT;   476 AA.
AC   Q6GMX1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073773; AAH73773.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   476 AA;  52286 MW;  622AABA5C62DDE9D CRC64;

  Query Match             84.8%;  Score 2029;  DB 2;  Length 476;
  Best Local Similarity   84.3%;  Pred. No. 1.4e-128;
  Matches  387;  Conservative   24;  Mismatches   34;  Indels   14;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS---YWIGWVRQMPGKGLEWMGIIYPGDSD 57
              :||| :||  : || ::| ::|  || | :|   ||  |:|| |||||||:| ||   |
Db         20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYW-SWIRQPPGKGLEWIGYIYYSGS- 77

Qy         58 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYW---------YFDLRG 108
              | |:|| : :|||| | | :   |: :|: |:|||:|:|     |          |:: |
Db         78 TYYNPSLKSRVTISLDTSKNQFSLKMNSVTAADTAVYFCARAGVWGSFRSWAIDGFNIWG 137

Qy        109 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 168
              :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 QGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 197

Qy        169 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 257

Qy        229 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        289 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        349 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        409 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||||||||
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Search completed: September  8, 2005, 00:54:03
Job time : 109.629 secs
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:01:25 ; Search time 30.6996 Seconds
(without alignments)
1086.923 Million cell updates/sec

Title: US-10-684-957-32
Perfect score: 2394
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2165	90.4	449	1	US-08-458-516-13	Sequence 13, Appl
2	2137.5	89.3	452	3	US-09-027-449-71	Sequence 71, Appl
3	2137.5	89.3	452	3	US-09-026-985-71	Sequence 71, Appl
4	2137.5	89.3	452	4	US-09-121-952A-71	Sequence 71, Appl
5	2137.5	89.3	452	4	US-09-234-340A-71	Sequence 71, Appl
6	2120	88.6	476	2	US-08-378-939-10	Sequence 10, Appl
7	2092	87.4	451	2	US-08-887-352B-18	Sequence 18, Appl
8	2092	87.4	451	3	US-09-109-207C-18	Sequence 18, Appl
9	2092	87.4	451	3	US-09-282-505-2	Sequence 2, Appli
10	2092	87.4	451	3	US-09-054-255-2	Sequence 2, Appli
11	2092	87.4	451	3	US-09-296-005-18	Sequence 18, Appl
12	2092	87.4	451	4	US-09-282-846-2	Sequence 2, Appli
13	2092	87.4	451	4	US-09-680-145-2	Sequence 2, Appli
14	2092	87.4	451	4	US-09-920-171-18	Sequence 18, Appl
15	2092	87.4	451	4	US-09-716-028-18	Sequence 18, Appl
16	2092	87.4	451	4	US-09-483-588-2	Sequence 2, Appli
17	2092	87.4	451	4	US-10-113-996-18	Sequence 18, Appl
18	2091	87.3	466	4	US-09-698-705-11	Sequence 11, Appl
19	2091	87.3	468	3	US-09-485-737B-67	Sequence 67, Appl
20	2091	87.3	468	4	US-10-071-485-67	Sequence 67, Appl
21	2091	87.3	711	3	US-09-485-737B-90	Sequence 90, Appl
22	2091	87.3	711	4	US-10-071-485-90	Sequence 90, Appl
23	2090	87.3	451	2	US-08-887-352B-14	Sequence 14, Appl
24	2090	87.3	451	2	US-08-887-352B-16	Sequence 16, Appl
25	2090	87.3	451	3	US-08-466-151-65	Sequence 65, Appl
26	2090	87.3	451	3	US-09-109-207C-14	Sequence 14, Appl
27	2090	87.3	451	3	US-09-109-207C-16	Sequence 16, Appl
28	2090	87.3	451	3	US-09-296-005-14	Sequence 14, Appl
29	2090	87.3	451	3	US-09-296-005-16	Sequence 16, Appl
30	2090	87.3	451	4	US-09-920-171-14	Sequence 14, Appl
31	2090	87.3	451	4	US-09-920-171-16	Sequence 16, Appl
32	2090	87.3	451	4	US-09-716-028-14	Sequence 14, Appl
33	2090	87.3	451	4	US-09-716-028-16	Sequence 16, Appl
34	2090	87.3	451	4	US-10-113-996-14	Sequence 14, Appl
35	2090	87.3	451	4	US-10-113-996-16	Sequence 16, Appl
36	2088.5	87.2	449	3	US-09-679-397-2	Sequence 2, Appli
37	2088.5	87.2	449	4	US-09-680-148-2	Sequence 2, Appli
38	2088.5	87.2	449	4	US-09-304-465A-2	Sequence 2, Appli
39	2081	86.9	472	4	US-09-301-593-43	Sequence 43, Appl
40	2072.5	86.6	467	3	US-09-049-672A-8	Sequence 8, Appli
41	2067	86.3	451	3	US-09-247-352-3	Sequence 3, Appli
42	2067	86.3	451	4	US-09-466-635-3	Sequence 3, Appli
43	2067	86.3	453	3	US-08-466-151-8	Sequence 8, Appli
44	2067	86.3	453	3	US-08-466-163B-8	Sequence 8, Appli
45	2067	86.3	453	4	US-09-802-096-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
;  GENERAL INFORMATION:
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Humanized Antibodies Reactive with
;    TITLE OF INVENTION:  GPIIB/IIIA
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,516
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,159
;      FILING DATE:  03-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-37-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  449 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-458-516-13

  Query Match             90.4%;  Score 2165;  DB 1;  Length 449;
  Best Local Similarity   89.5%;  Pred. No. 6.9e-163;
  Matches  402;  Conservative   24;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
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Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG--SGSYWYFDLRGRGTLVTVSSA 118
               :  |:|:||:: |:| :|||:: |||:: |||:|:|    |:| :|   |:|||||||||
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Qy        119 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        179 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        239 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 298
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Qy        299 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        359 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        419 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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RESULT 2
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/027,449
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074,330
;      FILING DATE:  22-Jan-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/038,664
;      FILING DATE:  21-Feb-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R3-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-027-449-71

  Query Match            89.3%;  Score 2137.5;  DB 3;  Length 452;
  Best Local Similarity   88.1%;  Pred. No. 1e-160;
  Matches  398;  Conservative   24;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
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Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----WYFDLRGRGTLVTV 115
               :  |:|: |:| | | :|||| :||:| |||:|||  | |     |:||: |:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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RESULT 3
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/026,985
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
```

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;      REFERENCE/DOCKET NUMBER:  P1085R3-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-026-985-71

  Query Match             89.3%;  Score 2137.5;  DB 3;  Length 452;
  Best Local Similarity   88.1%;  Pred. No. 1e-160;
  Matches  398;  Conservative   24;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||  : :|| ||::||  |||||:|::: |||| |||||||:| | | : :| |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----WYFDLRGRGTLVTV 115
              :  |:|: |:| | | :||||| :||:| |||:|||  | |      |:||: |:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 4
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952A
;      FILING DATE:  24-Jul-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-121-952A-71

  Query Match             89.3%;  Score 2137.5;  DB 4;  Length 452;
  Best Local Similarity   88.1%;  Pred. No. 1e-160;
  Matches  398;  Conservative   24;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||  : :|| ||::||  |||||:|::: |||| |||||||:| | | : :| |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----WYFDLRGRGTLVTV 115
              :  |:|: |:| | | :||||| :||:| |||:|||  | |      |:||: |:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
```

```
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/234,340A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952
;      FILING DATE:  24-Jul-1998
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-234-340A-71

  Query Match             89.3%;  Score 2137.5;  DB 4;  Length 452;
  Best Local Similarity   88.1%;  Pred. No. 1e-160;
  Matches  398;  Conservative   24;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||  : :|| ||::||  |||||:|::: |||| |||||||:| | | : :| |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----WYFDLRGRGTLVTV 115
              :  |:|: |:| | | :|||||  :||:| |||:|||  | |     |:||: |:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 6
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-10

  Query Match             88.6%;  Score 2120;  DB 2;  Length 476;
  Best Local Similarity   87.5%;  Pred. No. 2.7e-159;
  Matches  400;  Conservative   22;  Mismatches   25;  Indels   10;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ::|:||||||||||| |: :||| || :|::| | |||| ||:|||||| | |      |
Db         20 QMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYAISWVRQAPGQGLEWMGGIIPLFGTPTY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY----------WYFDLRGRG 110
              | :|||:|||:|||| |||::: :||:: |||:||| :  |           :||  |:|
Db         80 SQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCATDRYRQANFDRARVGWFDPWGQG 139

Qy        111 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 199

Qy        171 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 259

Qy        231 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 319

Qy        291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 350
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 379

Qy        351 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 410
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 439

Qy        411 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
                |||||||||||||||||||||||||||||||||||||
Db        440 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476


RESULT 7
US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5994511
;  GENERAL INFORMATION:
;    APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;    TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of
;    TITLE OF INVENTION:  Improving Polypeptides
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,352B
;      FILING DATE:  03-Jul-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-887-352B-18

  Query Match             87.4%;  Score 2092;  DB 2;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:|||  ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 8
US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
;  APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;  FILE REFERENCE:  P1123R1
;  CURRENT APPLICATION NUMBER: US/09/109,207C
;  CURRENT FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/051,554
;  PRIOR FILING DATE:  1997-07-03
;  NUMBER OF SEQ ID NOS:  44
; SEQ ID NO 18
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-18

  Query Match             87.4%;  Score 2092;  DB 3;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:|||  ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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```
RESULT 9
US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
;  APPLICANT: Esohe Ekinaduese Idusogie et al.
;  TITLE OF INVENTION: Polypeptide Variants
;  FILE REFERENCE: P1266R1
;  CURRENT APPLICATION NUMBER: US/09/282,505A
;  CURRENT FILING DATE: 1999-03-31
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Artificial Sequence
;   LOCATION: 1-451
;   OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

  Query Match             87.4%;  Score 2092;  DB 3;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:|||  ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 10
US-09-054-255-2
; Sequence 2, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
;  APPLICANT: Esohe Ekinaduese Idusogie et al.
;  TITLE OF INVENTION: Polypeptide Variants
;  FILE REFERENCE: P1266
;  CURRENT APPLICATION NUMBER: US/09/054,255
;  CURRENT FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: E27 anti-IgE antibody heavy chain
US-09-054-255-2

  Query Match             87.4%;  Score 2092;  DB 3;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:|||  ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 11
US-09-296-005-18
; Sequence 18, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
;  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
;  FILE REFERENCE: P1123Clr
;  CURRENT APPLICATION NUMBER: US/09/296,005
;  CURRENT FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 08/887,352
;  EARLIER FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 18
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-18

  Query Match             87.4%;  Score 2092;  DB 3;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
```

```
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:||| ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 12
US-09-282-846-2
; Sequence 2, Application US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/09/282,846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-2

Query Match 87.4%; Score 2092; DB 4; Length 451;
Best Local Similarity 87.6%; Pred. No. 4e-157;
Matches 397; Conservative 23; Mismatches 25; Indels 8; Gaps 4;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:||| ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

RESULT 13
US-09-680-145-2
; Sequence 2, Application US/09680145
; Patent No. 6538124
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/680,145
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/282,505
; PRIOR FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6538124
US-09-680-145-2

Query Match 87.4%; Score 2092; DB 4; Length 451;
Best Local Similarity 87.6%; Pred. No. 4e-157;
Matches 397; Conservative 23; Mismatches 25; Indels 8; Gaps 4;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:||| ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
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Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 14
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
;  APPLICANT: Lowman, Henry B.
;  APPLICANT:  Presta, Leonard G.
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Lowe, John
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;  FILE REFERENCE: P1123C2US
;  CURRENT APPLICATION NUMBER: US/09/920,171
;  CURRENT FILING DATE:  2001-08-01
;  PRIOR APPLICATION NUMBER: US 08/887,352
;  PRIOR FILING DATE: 1997-07-02
;  PRIOR APPLICATION NUMBER: US 09/296,005
;  PRIOR FILING DATE: 1999-04-21
;  NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

  Query Match             87.4%;  Score 2092;  DB 4;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:||| ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 15
US-09-716-028-18
; Sequence 18, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
;  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
;  FILE REFERENCE: P1123R1
;  CURRENT APPLICATION NUMBER: US/09/716,028
;  CURRENT FILING DATE:  2000-11-17
;  PRIOR APPLICATION NUMBER: US 09/109,207
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/051,554
;  PRIOR FILING DATE: 1997-07-03
;  NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-18

  Query Match             87.4%;  Score 2092;  DB 4;  Length 451;
  Best Local Similarity   87.6%;  Pred. No. 4e-157;
  Matches  397;  Conservative   23;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTS-YWIGWVRQMPGKGLEWMGII-YPGDSDT 58
              |||||:||  : :|| ||::||  |||| || |   |:|| |||||||:  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS----YWYFDLRGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:||| ||    :|:| : |:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


Search completed: September  8, 2005, 00:15:44
Job time : 31.6996 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:11:22 ; Search time 120.437 Seconds
(without alignments)
1435.455 Million cell updates/sec

Title: US-10-684-957-32
Perfect score: 2394
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2394	100.0	447	8	ADS87939	Ads87939 Anti-IFN-
2	2394	100.0	447	8	ADS94936	Ads94936 Anti-IFN-
3	2386	99.7	447	8	ADS87926	Ads87926 Anti-IFN-
4	2386	99.7	447	8	ADS94923	Ads94923 Anti-IFN-
5	2383	99.5	447	8	ADS87928	Ads87928 Anti-IFN-
6	2383	99.5	447	8	ADS94925	Ads94925 Anti-IFN-
7	2360	98.6	447	8	ADS87924	Ads87924 Anti-IFN-
8	2360	98.6	447	8	ADS94921	Ads94921 Anti-IFN-
9	2296.5	95.9	468	8	ADR46819	Adr46819 Human ant
10	2296.5	95.9	613	8	ADR46827	Adr46827 Human bet
11	2274	95.0	474	4	AAU14177	Aau14177 Human nov
12	2259.5	94.4	467	8	ADM41567	Adm41567 Anti-inte
13	2180.5	91.1	450	8	ADS18704	Ads18704 Protein s
14	2175.5	90.9	450	8	ADS18702	Ads18702 Protein s
15	2175.5	90.9	450	8	ADS18708	Ads18708 Protein s
16	2174.5	90.8	450	8	ADS18710	Ads18710 Protein s
17	2174	90.8	470	3	AAW90936	Aaw90936 Humanised
18	2174	90.8	470	5	ABB74945	Abb74945 Humanised
19	2170	90.6	470	3	AAW90935	Aaw90935 Humanised
20	2170	90.6	470	5	ABB74904	Abb74904 Mouse hum
21	2169	90.6	470	3	AAW90934	Aaw90934 Humanised
22	2169	90.6	470	5	ABB74903	Abb74903 Mouse hum
23	2167	90.5	470	3	AAW90933	Aaw90933 Humanised
24	2167	90.5	470	5	ABB74902	Abb74902 Humanised
25	2166.5	90.5	450	8	ADS18706	Ads18706 Protein s
26	2166	90.5	470	2	AAW83037	Aaw83037 Anti-Fas
27	2166	90.5	470	3	AAB14779	Aab14779 Humanised
28	2166	90.5	470	3	AAW90929	Aaw90929 Humanised
29	2166	90.5	470	5	ABB74944	Abb74944 Humanised
30	2166	90.5	470	5	ABB74898	Abb74898 Humanised
31	2165	90.4	449	2	AAR43339	Aar43339 Completel
32	2165	90.4	449	2	AAW49816	Aaw49816 Amino aci
33	2164.5	90.4	471	8	ADP79584	Adp79584 2H7.v16 H
34	2160	90.2	448	6	ABR55871	Abr55871 Human imm
35	2160	90.2	448	8	ADN49728	Adn49728 Human imm
36	2158.5	90.2	731	4	AAM52156	Aam52156 Humanised
37	2158.5	90.2	741	4	AAM52159	Aam52159 Humanised
38	2158	90.1	470	2	AAW83036	Aaw83036 Anti-Fas
39	2158	90.1	470	3	AAB14776	Aab14776 Humanised
40	2158	90.1	470	3	AAW90926	Aaw90926 Humanised
41	2158	90.1	470	5	ABB74941	Abb74941 Humanised
42	2158	90.1	470	5	ABB74895	Abb74895 Humanised
43	2155.5	90.0	445	8	ADJ11308	Adj11308 BHA10 VH#
44	2155.5	90.0	464	8	ADJ11354	Adj11354 BHA10 VL#
45	2154	90.0	451	8	ADF11670	Adf11670 anti-CD11

ALIGNMENTS

RESULT 1
ADS87939
ID ADS87939 standard; protein; 447 AA.
XX
AC ADS87939;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 32; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36

CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 2394; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 2
ADS94936
ID ADS94936 standard; protein; 447 AA.
XX
AC ADS94936;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 32; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 2394; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
```

```
Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 3
ADS87926
ID ADS87926 standard; protein; 447 AA.
XX
AC ADS87926;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 19; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

```
  Query Match             99.7%;  Score 2386;  DB 8;  Length 447;
  Best Local Similarity   99.8%;  Pred. No. 8e-137;
  Matches  446;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 4
ADS94923
ID ADS94923 standard; protein; 447 AA.
XX
AC ADS94923;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.

XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 19; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 99.7%; Score 2386; DB 8; Length 447;
Best Local Similarity 99.8%; Pred. No. 8e-137;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 5
ADS87928
ID ADS87928 standard; protein; 447 AA.
XX
AC ADS87928;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 21; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 99.5%; Score 2383; DB 8; Length 447;
Best Local Similarity 99.6%; Pred. No. 1.2e-136;
Matches 445; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
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```
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 6
ADS94925
ID ADS94925 standard; protein; 447 AA.
XX
AC ADS94925;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 21; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 99.5%; Score 2383; DB 8; Length 447;
Best Local Similarity 99.6%; Pred. No. 1.2e-136;
Matches 445; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 7
ADS87924
ID ADS87924 standard; protein; 447 AA.
XX
AC ADS87924;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;

```
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 12; SEQ ID NO 17; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             98.6%;  Score 2360;  DB 8;  Length 447;
  Best Local Similarity   99.1%;  Pred. No. 3e-135;
  Matches  443;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||:|||| ||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 8
ADS94921
ID   ADS94921 standard; protein; 447 AA.
XX
AC   ADS94921;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 14; SEQ ID NO 17; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
```

CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 98.6%; Score 2360; DB 8; Length 447;
Best Local Similarity 99.1%; Pred. No. 3e-135;
Matches 443; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||:|||| ||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 9
ADR46819
ID ADR46819 standard; protein; 468 AA.
XX
AC ADR46819;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human antibody B11 heavy chain variable region protein SEQ ID NO:2.
XX
KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; heavy chain variable region.
XX
OS Homo sapiens.
XX
PN WO2004074432-A2.
XX
PD 02-SEP-2004.
XX
PF 30-JAN-2004; 2004WO-US002725.
XX
PR 31-JAN-2003; 2003US-0443979P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Keler T, Endres M, He L, Ramakrishna V;
XX
DR WPI; 2004-635555/61.
DR N-PSDB; ADR46818.
XX
PT New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.
XX
PS Claim 13; SEQ ID NO 2; 82pp; English.
XX
CC The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human antibody B11 heavy chain
CC variable region, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 468 AA;

Query Match 95.9%; Score 2296.5; DB 8; Length 468;
Best Local Similarity 96.2%; Pred. No. 2.3e-131;
Matches 434; Conservative 3; Mismatches 5; Indels 9; Gaps 2;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||:||||||| |||:||||||||||||||||||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG----SYWYFDLRGRGTLVTVS 116
              |||||||||||||||||||||||||||||||||||  |    ||     |:|||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDRGVDYW-----GQGTLVTVS 134

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        135 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 194

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 254

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 314

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 374

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 434

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        435 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 10
ADR46827
ID   ADR46827 standard; protein; 613 AA.
XX
AC   ADR46827;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW   CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW   melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW   antibody B11; betahCG-B11 molecular conjugate; fusion protein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004074432-A2.
XX
PD   02-SEP-2004.
XX
PF   30-JAN-2004; 2004WO-US002725.
XX
PR   31-JAN-2003; 2003US-0443979P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T,  Endres M,  He L,  Ramakrishna V;
XX
DR   WPI; 2004-635555/61.
DR   N-PSDB; ADR46826.
XX
PT   New molecular conjugate having a monoclonal antibody that binds to human
PT   APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT   cytotoxic T cell response in cancers and infectious diseases.
XX
PS   Example 1; SEQ ID NO 10; 82pp; English.
XX
CC   The present invention describes a molecular conjugate comprising a
CC   monoclonal antibody that binds to human antigen presenting cells (APCs)
CC   linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC   comprises a heavy and/or light chain variable region derived from a human
CC   VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC   of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC   described: (1) a molecular conjugate comprising a human antibody heavy
CC   chain and a human antibody light chain, where either or both chains are
CC   linked to betahCG; (2) a molecular conjugate comprising a human single
CC   chain antibody that binds to human APCs linked to betahCG, where the
CC   conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC   (ADR46829); (3) a composition comprising any of the molecular conjugates
CC   as described above, and a carrier, optionally in combination with an
CC   adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC   against betahCG, comprising contacting any of the molecular conjugates
CC   described above with APCs such that the antigen is processed and
CC   presented to T cells in a manner which induces or enhances a T cell-
CC   mediated response against the antigen; (5) immunising a subject
CC   comprising administering any of the molecular conjugates described above,
CC   optionally in combination with an adjuvant, a cytokine which stimulates
CC   proliferation of dendritic cells and/or an immunostimulatory agent; and
CC   (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC   comprising forming a conjugate of the antigen and a monoclonal antibody
CC   which binds to APCs, and contacting the conjugate either in vivo or ex
CC   vivo with APCs such that the antigen is internalised, processed and
CC   presented to T cells in a manner which induces or enhances a cytotoxic T
CC   cell response against the antigen. The molecular conjugate has
CC   cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC   virucide and antimalarial activities, and can be used as a CD8 agonist,
CC   and in vaccines. The methods and compositions of the present invention
CC   are useful for inducing a cytotoxic T cell response, and in particular
CC   for treating autoimmune disorders, cancers and infectious diseases by
CC   eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC   including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC   herpes. The present sequence represents a human betahCG-B11 molecular
CC   conjugate, which is used in the exemplification of the present invention.
XX
SQ   Sequence 613 AA;

  Query Match             95.9%;  Score 2296.5;  DB 8;  Length 613;
  Best Local Similarity   96.2%;  Pred. No. 3.1e-131;
  Matches  434;  Conservative    3;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||| |||:|||||||||||||||||||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG----SYWYFDLRGRGTLVTVS 116
              |||||||||||||||||||||||||||||||||  |    ||     |:|||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDRGVDYW-----GQGTLVTVS 134

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 194

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 254

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 314

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 374

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 434

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        435 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 11
AAU14177
ID   AAU14177 standard; protein; 474 AA.
XX
```

```
AC   AAU14177;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #48.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002623.
XX
PR   25-JAN-2000; 2000US-00491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22482.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage.
XX
PS   Example 4; Page 554-555; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human proteins or
CC   their active domains. The polypeptides, polynucleotides and antibodies
CC   raised against the polypeptides are used in a method of treatment of a
CC   mammal and prevention of disorders caused by the aberrant protein
CC   expression or activity. The polypeptides can be used as molecular weight
CC   markers, food supplements, and in antibody production. The polypeptides
CC   are used to identify compounds which bind to the polypeptides.
CC   Polynucleotides of the invention are used as probes and primers, for
CC   sequencing, for chromosome or gene mapping, in the production of
CC   recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC   therapy. Polypeptides of the invention can be used to target drugs to a
CC   tumour, in assays to determine biological activity, to raise
CC   antibodies/elicit an immune response, to determine quantitative protein
CC   levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC   versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC   diseases, nervous system disorders, and infection. The present sequence
CC   represents a protein of the invention
XX
SQ   Sequence 474 AA;

  Query Match             95.0%;  Score 2274;  DB 4;  Length 474;
  Best Local Similarity   94.1%;  Pred. No. 5.4e-130;
  Matches  428;  Conservative    8;  Mismatches   11;  Indels    8;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||||||||||||||:||||||||||: ||: |||| | ||| ||||||||||||||
Db         20 EVQLVQSGAEVKKPGESVKISCKGSGYSFSDYWVAWVRQSPDKGLAWMGIIYPGDSDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG------SYWYF--DLRGRGTL 112
                ||||||||||||||||||||||||| ||||||||  |      || |:  |: ||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKDSDTAMYYCARGARGTAPSYHYYGLDVWGRGTS 139

Qy        113 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199

Qy        173 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 232
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        200 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259

Qy        233 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 319

Qy        293 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 379

Qy        353 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 412
              |||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 439

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||||
Db        440 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474


RESULT 12
ADM41567
ID   ADM41567 standard; protein; 467 AA.
XX
AC   ADM41567;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Anti-interleukin-1 receptor type 1 antibody heavy chain.
XX
KW   Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW   antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW   protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW   analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW   anticonvulsant; dermatological; antigout; antiparkinsonian; antidiabetic;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004022718-A2.
XX
PD   18-MAR-2004.
XX
PF   05-SEP-2003; 2003WO-US027978.
XX
PR   06-SEP-2002; 2002US-0408719P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Varnum B,  Vezina C,  Witte A,  Qian X,  Martin F,  Huang H;
PI   Elliott G;
XX
DR   WPI; 2004-248462/23.
DR   N-PSDB; ADM41566.
XX
PT   Isolated human antibody that specifically binds interleukin-1 receptor
PT   type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
PT   rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
PS   Claim 3; SEQ ID NO 32; 179pp; English.
XX
CC   The present sequence is that of a human anti-interleukin-1 receptor type
CC   1 (IL-1R1) monoclonal antibody (MAb) heavy chain. The invention provides
CC   antibodies that comprise this sequence. Human MAbs to IL-1R1 were
CC   prepared using the HCo7 strain of transgenic mice, which expresses human
```

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CC   antibody genes. These mice were immunised with purified recombinant IL-
CC   1R1, and splenocytes from immunised mice were fused to a mouse myeloma
CC   cell line to generate hybridomas. Hybridomas which secreted a MAb that
CC   bound with high avidity to IL-1R1 were selected. The MAbs inhibit IL-1
CC   signalling by competing with IL-1beta and IL-1alpha binding to IL-1R.
CC   These MAbs, as well as single chain antibodies single chain Fv
CC   antibodies, Fab antibodies, Fab' antibodies and (Fab')2 antibodies
CC   derived from them, are used in methods of treating IL-1 mediated diseases
CC   or for detecting the amount of IL-1R1 in a sample. IL-1 mediated diseases
CC   include acute pancreatitis, amyotrophic lateral sclerosis, Alzheimer's
CC   disease, cachexia, anorexia, asthma, atherosclerosis, autoimmune
CC   vasculitis, chronic fatigue syndrome, Clostridium associated illnesses,
CC   coronary conditions, cancer including leukaemia and tumour metastasis,
CC   diabetes, endometriosis, fever, fibromyalgia, glomerulonephritis, graft
CC   versus host disease, osteoarthritis, rheumatoid arthritis, inflammatory
CC   eye disease, ischaemia, Kawasaki's disease, learning impairment, lung
CC   diseases, multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's
CC   disease, periodontal disease, pre-term labour, psoriasis, reperfusion
CC   injury, septic shock, side effects of radiation therapy, temporal
CC   mandibular joint disease, sleep disturbance, uveitis, or an inflammatory
CC   condition resulting from strain, sprain, cartilage damage, trauma,
CC   orthopaedic surgery, infection or other disease processes.
XX
SQ   Sequence 467 AA;

  Query Match             94.4%;  Score 2259.5;  DB 8;  Length 467;
  Best Local Similarity   95.1%;  Pred. No. 4e-129;
  Matches  426;  Conservative    6;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ||||:|||||||||||||||||||||||: :|| ||||||||||||||:|| |||||
Db         20 EVQLMQSGAEVKKPGESLKISCKGSGYSFSFHWIAWVRQMPGKGLEWMGIIHPGASDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYWYFDLRGRGTLVTVSSAS 119
              |||||||||||||| | |  ||||||||||||||:|       |||  |:||||||||||
Db         80 SPSFQGQVTISADNSNSATYLQWSSLKASDTAMYFCARQRELDYFDYWGQGTLVTVSSAS 139

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 199

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 259

Qy        240 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 319

Qy        300 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 379

Qy        360 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 439

Qy        420 GNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||
Db        440 GNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 13
ADS18704
ID   ADS18704 standard; protein; 450 AA.
XX
AC   ADS18704;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Protein sequence of human W17-IgG1 heavy chain.
XX
KW   Antibody; humanised; complementarity determining region; CDR; CDR1; CDR2;
KW   CDR3; W17-IgG1 heavy chain; interleukin -1 beta; IL-1 beta; cytokine;
KW   bone destruction; cartilage destruction; rheumatoid arthritis;
KW   osteoarthritis; clinical efficacy; neuro-inflammation; stroke; ischaemic;
KW   excitotoxic; traumatic head injury; inflammatory disorder; IgG; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "This specification states that there is
FT                   elimination of deamidation at this position, however,
FT                   this residue is a Serine and not an Asparagine or
FT                   Glutamine"
XX
PN   WO2004067568-A2.
XX
PD   12-AUG-2004.
XX
PF   21-JAN-2004; 2004WO-US000019.
XX
PR   24-JAN-2003; 2003US-0442798P.
XX
PA   (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI   Dickinson CD,  Vasserot AP,  Watkins JD,  Lu J;
XX
DR   WPI; 2004-580977/56.
XX
PT   New isolated antibodies that specifically bind mature human IL-1 beta,
PT   useful for treating diseases such as rheumatoid arthritis, osteoarthritis
PT   or neuroinflammation, or for inhibiting cartilage destruction.
XX
PS   Claim 5; SEQ ID NO 47; 79pp; English.
XX
CC   The present invention encompasses humanised IL-1 beta antibodies. These
CC   antibodies are high affinity antibodies with improved stability, reduced
CC   deamidation and highly specific for IL-1 beta compared to the native
CC   antibody. They have potent IL-1 beta neutralising activity. The increased
CC   potency of an existing antibody is achieved through selective changes to
CC   one or more amino acids. The property of the antibodies of the invention
CC   resides primarily in the variable regions or complementarity determining
CC   regions (CDR) of the antibody. The proposed antibodies are comprised of
CC   light chain (CDR1, CDR2 and CDR3) and heavy chain (CDR1, CDR2 and CDR3)
CC   antibody. Interleukin -1 beta is a pro-inflammatory cytokine which is the
CC   primary mediator of bone and cartilage destruction. The over-production
CC   of the IL-1 beta has been implicated in the pathogenesis of a variety of
CC   diseases (rheumatoid arthritis, osteoarthritis, asthma, neuro-
CC   inflammation, graft versus host disease, Crohn's disease, inflammatory
CC   bowel disease, multiple sclerosis, Parkinson's and Alzheimer's disease
CC   etc.). An effective amount of the IL-1 beta antibodies of the present
CC   invention provides clinical efficacy without intolerable side effects or
CC   toxicity. The antibodies are also useful for manufacturing a medicament
CC   for the treatment of rheumatoid arthritis and osteoarthritis. It can be
CC   used to inhibit cartilage destruction and neuro-inflammation (which is
CC   associated with stroke or ischaemic, excitotoxic, or traumatic head
CC   injury). The IL-1 beta antibodies of the invention are preferably used to
CC   treat rheumatoid arthritis (RA), osteoarthritis (OA) and neuro-
CC   inflammation. The IL-1 beta antibodies of the invention can be used alone
CC   or in combination DMARDS (disease modifying antirheumatic drugs) to
CC   reduce IL-1 beta protein levels in plasma. The invention provides the
CC   polynucleotide sequences which encode the antibodies against IL-1 beta.
CC   It also provides the methods for using these antibodies for the treatment
CC   of IL-1 beta related inflammatory disorders. The isolated antibodies of
CC   the invention are selected from the group IgG1 and IgG4. IgG antibodies
CC   are the most abundant immunoglobulin and has the longest half-life in
CC   serum compared to other immunoglobulin. Unlike other immunoglobulins IgG
CC   is efficiently recirculated. The presented protein sequence is the human
CC   W17-IgG1 heavy chain.
XX
SQ   Sequence 450 AA;

  Query Match             91.1%;  Score 2180.5;  DB 8;  Length 450;
  Best Local Similarity   90.9%;  Pred. No. 2.4e-124;
```

```
  Matches  409;  Conservative   15;  Mismatches   23;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|  ||| |||| ||:|||||| | ||  |  |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFDRYWIEWVRQAPGQGLEWMGEILPGSGDINY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWY---FDLRGRGTLVTVSS 117
              :  |:|:|||:|||| ||||:: |||:: |||:|||    | |   ||| |:||||||||
Db         61 NEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARMYYDYDQGFDLWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450


RESULT 14
ADS18702
ID   ADS18702 standard; protein; 450 AA.
XX
AC   ADS18702;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Protein sequence of human W13-heavy chain.
XX
KW   Antibody; humanised; complementarity determining region; CDR; CDR1; CDR2;
KW   CDR3; W13 heavy chain; interleukin -1 beta; IL-1 beta; cytokine;
KW   bone destruction; cartilage destruction; rheumatoid arthritis;
KW   osteoarthritis; clinical efficacy; neuro-inflammation; stroke; ischaemic;
KW   excitotoxic; traumatic head injury; inflammatory disorder; IgG; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "This specification states that there is
FT                   elimination of deamidation at this position, however,
FT                   this residue is a Serine and not an Asparagine or
FT                   Glutamine"
XX
PN   WO2004067568-A2.
XX
PD   12-AUG-2004.
XX
PF   21-JAN-2004; 2004WO-US000019.
XX
PR   24-JAN-2003; 2003US-0442798P.
XX
PA   (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI   Dickinson CD,  Vasserot AP,  Watkins JD,  Lu J;
XX
DR   WPI; 2004-580977/56.
XX
PT   New isolated antibodies that specifically bind mature human IL-1 beta,
PT   useful for treating diseases such as rheumatoid arthritis, osteoarthritis
PT   or neuroinflammation, or for inhibiting cartilage destruction.
XX
PS   Claim 9; SEQ ID NO 45; 79pp; English.
XX
CC   The present invention encompasses humanised IL-1 beta antibodies. These
CC   antibodies are high affinity antibodies with improved stability, reduced
CC   deamidation and highly specific for IL-1 beta compared to the native
CC   antibody. They have potent IL-1 beta neutralising activity. The increased
CC   potency of an existing antibody is achieved through selective changes to
CC   one or more amino acids. The property of the antibodies of the invention
CC   resides primarily in the variable regions or complementarity determining
CC   regions (CDR) of the antibody. The proposed antibodies are comprised of
CC   light chain (CDR1, CDR2 and CDR3) and heavy chain (CDR1, CDR2 and CDR3)
CC   antibody. Interleukin -1 beta is a pro-inflammatory cytokine which is the
CC   primary mediator of bone and cartilage destruction. The over-production
CC   of the IL-1 beta has been implicated in the pathogenesis of a variety of
CC   diseases (rheumatoid arthritis, osteoarthritis, asthma, neuro-
CC   inflammation, graft versus host disease, Crohn's disease, inflammatory
CC   bowel disease, multiple sclerosis, Parkinson's and Alzheimer's disease
CC   etc.). An effective amount of the IL-1 beta antibodies of the present
CC   invention provides clinical efficacy without intolerable side effects or
CC   toxicity. The antibodies are also useful for manufacturing a medicament
CC   for the treatment of rheumatoid arthritis and osteoarthritis. It can be
CC   used to inhibit cartilage destruction and neuro-inflammation (which is
CC   associated with stroke or ischaemic, excitotoxic, or traumatic head
CC   injury). The IL-1 beta antibodies of the invention are preferably used to
CC   treat rheumatoid arthritis (RA), osteoarthritis (OA) and neuro-
CC   inflammation. The IL-1 beta antibodies of the invention can be used alone
CC   or in combination DMARDS (disease modifying antirheumatic drugs) to
CC   reduce IL-1 beta protein levels in plasma. The invention provides the
CC   polynucleotide sequences which encode the antibodies against IL-1 beta.
CC   It also provides the methods for using these antibodies for the treatment
CC   of IL-1 beta related inflammatory disorders. The isolated antibodies of
CC   the invention are selected from the group IgG1 and IgG4. IgG antibodies
CC   are the most abundant immunoglobulin and has the longest half-life in
CC   serum compared to other immunoglobulin. Unlike other immunoglobulins IgG
CC   is efficiently recirculated. The presented protein sequence is the human
CC   W13-heavy chain.
XX
SQ   Sequence 450 AA;

  Query Match             90.9%;  Score 2175.5;  DB 8;  Length 450;
  Best Local Similarity   90.7%;  Pred. No. 4.9e-124;
  Matches  408;  Conservative   15;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|  ||| |||| ||:|||||| | ||  |  |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFDRYWIEWVRQAPGQGLEWMGEILPGSGDINY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWY---FDLRGRGTLVTVSS 117
              :  |:|:|||:|||| ||||:: |||:: |||:|||    | |   ||  |:||||||||
Db         61 NEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARMYYDYDQGFDYWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
                ||||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450


RESULT 15
ADS18708
ID   ADS18708 standard; protein; 450 AA.
XX
AC   ADS18708;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Protein sequence of human W20-heavy chain.
XX
KW   Antibody; humanised; complementarity determining region; CDR; CDR1; CDR2;
KW   CDR3; W20-heavy chain; interleukin -1 beta; IL-1 beta; cytokine;
KW   bone destruction; cartilage destruction; rheumatoid arthritis;
KW   osteoarthritis; clinical efficacy; neuro-inflammation; stroke; ischaemic;
KW   excitotoxic; traumatic head injury; inflammatory disorder; IgG; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "This specification states that there is
FT                   elimination of deamidation at this position, however,
FT                   this residue is a Serine and not an Asparagine or
FT                   Glutamine"
XX
PN   WO2004067568-A2.
XX
PD   12-AUG-2004.
XX
PF   21-JAN-2004; 2004WO-US000019.
XX
PR   24-JAN-2003; 2003US-0442798P.
XX
PA   (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI   Dickinson CD,  Vasserot AP,  Watkins JD,  Lu J;
XX
DR   WPI; 2004-580977/56.
XX
PT   New isolated antibodies that specifically bind mature human IL-1 beta,
PT   useful for treating diseases such as rheumatoid arthritis, osteoarthritis
PT   or neuroinflammation, or for inhibiting cartilage destruction.
XX
PS   Claim 15; SEQ ID NO 51; 79pp; English.
XX
CC   The present invention encompasses humanised IL-1 beta antibodies. These
CC   antibodies are high affinity antibodies with improved stability, reduced
CC   deamidation and highly specific for IL-1 beta compared to the native
CC   antibody. They have potent IL-1 beta neutralising activity. The increased
CC   potency of an existing antibody is achieved through selective changes to
CC   one or more amino acids. The property of the antibodies of the invention
CC   resides primarily in the variable regions or complementarity determining
CC   regions (CDR) of the antibody. The proposed antibodies are comprised of
CC   light chain (CDR1, CDR2 and CDR3) and heavy chain (CDR1, CDR2 and CDR3)
CC   antibody. Interleukin -1 beta is a pro-inflammatory cytokine which is the
CC   primary mediator of bone and cartilage destruction. The over-production
CC   of the IL-1 beta has been implicated in the pathogenesis of a variety of
CC   diseases (rheumatoid arthritis, osteoarthritis, asthma, neuro-
CC   inflammation, graft versus host disease, Crohn's disease, inflammatory
CC   bowel disease, multiple sclerosis, Parkinson's and Alzheimer's disease
CC   etc.). An effective amount of the IL-1 beta antibodies of the present
CC   invention provides clinical efficacy without intolerable side effects or
CC   toxicity. The antibodies are also useful for manufacturing a medicament
CC   for the treatment of rheumatoid arthritis and osteoarthritis. It can be
CC   used to inhibit cartilage destruction and neuro-inflammation (which is
CC   associated with stroke or ischaemic, excitotoxic, or traumatic head
CC   injury). The IL-1 beta antibodies of the invention are preferably used to
CC   treat rheumatoid arthritis (RA), osteoarthritis (OA) and neuro-
CC   inflammation. The IL-1 beta antibodies of the invention can be used alone
CC   or in combination DMARDS (disease modifying antirheumatic drugs) to
CC   reduce IL-1 beta protein levels in plasma. The invention provides the
CC   polynucleotide sequences which encode the antibodies against IL-1 beta.
CC   It also provides the methods for using these antibodies for the treatment
CC   of IL-1 beta related inflammatory disorders. The isolated antibodies of
CC   the invention are selected from the group IgG1 and IgG4. IgG antibodies
CC   are the most abundant immunoglobulin and has the longest half-life in
CC   serum compared to other immunoglobulin. Unlike other immunoglobulins IgG
CC   is efficiently recirculated. The presented protein sequence is the human
CC   W20-heavy chain.
XX
SQ   Sequence 450 AA;

  Query Match             90.9%;  Score 2175.5;  DB 8;  Length 450;
  Best Local Similarity   90.7%;  Pred. No. 4.9e-124;
  Matches  408;  Conservative   15;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| |||:|  ||| |||| ||:|||||| | ||  |  |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFDRYWIEWVRQAPGQGLEWMGEILPGSGDINY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWY---FDLRGRGTLVTVSS 117
              :  |:|:|||:|||| ||||:: |||:: |||:|||    | |   ||  |:||||||||
Db         61 NEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARMYYDYDQGFDYWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450


Search completed: September  8, 2005, 00:42:59
Job time : 122.437 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:34:28 ; Search time 24.2898 Seconds
(without alignments)
1770.656 Million cell updates/sec

Title: US-10-684-957-32
Perfect score: 2394
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1767	73.8	330	1	GHHU	Ig gamma-1 chain C
2	1630.5	68.1	377	2	A23511	Ig gamma-3 chain C
3	1628.5	68.0	377	2	A60764	Ig gamma-3 chain C
4	1604	67.0	326	1	G2HU	Ig gamma-2 chain C
5	1590.5	66.4	327	1	G4HU	Ig gamma-4 chain C
6	1469	61.4	446	2	S40295	Ig gamma-2a chain
7	1468.5	61.3	469	2	S37483	Ig gamma-2a chain
8	1436	60.0	374	2	S69339	Ig heavy chain V r
9	1421	59.4	470	2	S22080	Ig heavy chain pre
10	1409.5	58.9	444	2	PC4436	monoclonal antibod
11	1402	58.6	472	2	S31459	Ig gamma-1 chain -
12	1393.5	58.2	475	2	S01321	Ig gamma-2b chain
13	1385	57.9	474	1	G2MS11	Ig gamma-2b chain
14	1263	52.8	328	2	I47159	Ig gamma 2a chain
15	1260	52.6	255	4	S31866	Ig gamma-1 chain C
16	1257	52.5	328	2	I47160	Ig gamma 2b chain
17	1254	52.4	234	2	PT0207	Ig gamma chain C r
18	1231	51.4	328	2	I47158	Ig gamma 1 chain c
19	1230.5	51.4	323	1	GHRB	Ig gamma chain C r
20	1227	51.3	328	2	I47161	Ig gamma 3 chain c
21	1216.5	50.8	329	1	G2GP	Ig gamma-2 chain C
22	1161.5	48.5	308	2	C30554	Ig heavy chain C r
23	1152	48.1	326	2	PS0017	Ig gamma-1 chain C
24	1151	48.1	289	1	G3HUWI	Ig gamma-3 heavy c
25	1146.5	47.9	333	2	PS0018	Ig gamma-2b chain
26	1142	47.7	324	1	G1MS	Ig gamma-1 chain C
27	1141	47.7	329	1	G3MSC	Ig gamma-3 chain C
28	1137	47.5	393	1	G1MSM	Ig gamma-1 chain C
29	1130	47.2	398	1	G3MSM	Ig gamma-3 chain C
30	1126	47.0	330	1	G2MSA	Ig gamma-2a chain
31	1123.5	46.9	335	1	G2MSAB	Ig gamma-2a chain
32	1121	46.8	399	1	G2MSAM	Ig gamma-2a chain
33	1118.5	46.7	329	2	S00847	Ig gamma-2c chain
34	1112	46.4	322	2	PS0019	Ig gamma-2a chain
35	1092.5	45.6	327	2	S06611	Ig gamma-2 chain C
36	1082	45.2	405	1	G2MSBM	Ig gamma-2b chain
37	1066	44.5	277	2	I47162	Ig gamma 4 chain c
38	969	40.5	548	2	S38864	Ig epsilon chain C
39	935.5	39.1	549	2	S04845	Ig heavy chain pre
40	809.5	33.8	241	2	S69131	Ig heavy chain (DO
41	798	33.3	627	2	S14683	Ig mu chain precur
42	782	32.7	246	2	S38950	Ig gamma chain - m
43	774	32.3	220	2	A49444	Ig gamma-1 heavy c
44	754.5	31.5	572	2	B46529	Ig Y heavy chain (
45	722.5	30.2	249	2	S69340	Ig heavy chain VHI

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             73.8%;  Score 1767;  DB 1;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-96;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             68.1%;  Score 1630.5;  DB 2;  Length 377;
  Best Local Similarity   82.0%;  Pred. No. 2.2e-88;
  Matches  309;  Conservative   10;  Mismatches   11;  Indels   47;  Gaps    1;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              |||||||||||||  |:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 215
              ||||||||||||||||||| |||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy        216 -------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 250
                                        ||||||    || ||||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        251 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 310
              ||||||||||||||||||||||:| ||||||||||||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        311 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 370
              |||||||||||||||||||||||||| |||||||||||||:|:||||||||||
Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        371 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 430
              |||||||||||:|||||||  ||||:||||||||||||||||||||:||||||||
Db        301 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy        431 ALHNHYTQKSLSLSPGK 447
              |||| :||||||||||
Db        361 ALHNRFTQKSLSLSPGK 377


RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
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F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 1628.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 2.9e-88;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

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Qy      118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
            |||||||||||||| |:||||||||||||||||||||||||||||||||||||||||||||
Db        1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy      178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 215
            |||||||||||||||||||| ||||||||||||||:|
Db       61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy      216 -------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 250
                                      ||||||    || ||||||||||||||||||||
Db      121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy      251 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 310
            |||||||||||||||||||||:| ||||||||||||||||||||:||||||||||
Db      181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy      311 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 370
            |||||||||||||||||||||||||| ||||||||||||||:|:||||||||||||
Db      241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy      371 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 430
            |||||||||||||:|||||| ||||||||||||||||:|||||||||:||||||||||
Db      301 GFYPSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

Qy      431 ALHNHYTQKSLSLSPGK 447
            |||| :||||||||||
Db      361 ALHNRFTQKSLSLSPGK 377
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RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.0%; Score 1604; DB 1; Length 326;
Best Local Similarity 91.2%; Pred. No. 6.6e-87;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

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Qy      118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
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Db        1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy      178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
            |||||||||||||: ||||| |||:|||||||||| || | | :  |||||||  : |
Db       61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy      238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
            ||||||||||||||||||||||||||||||||||:||||||||||||||||||:|
Db      117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy      298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
            ||:|||||||:|||||||||||||| |||||||||| |||||||||||:|
Db      177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy      358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
            :||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db      237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy      418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
            ||||||||||||||||||||||||||||||
Db      297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
```

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

```
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             66.4%;  Score 1590.5;  DB 1;  Length 327;
  Best Local Similarity   90.9%;  Pred. No. 4.1e-86;
  Matches  300;  Conservative   12;  Mismatches   15;  Indels    3;  Gaps    1;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||| |:||| ||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||:|| |||:||||||||:|| |       || ||||| |||
Db         61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              |||||||||||||||||||||||||||| |||||:|||||||||||||||||||||:|
Db        118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              |||||||||||||||||||||||||||| ||: ||||||||||||||||||||::|
Db        178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              :|||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |:|||||||||||||||||||||||| ||
Db        298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 6
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
A;Cross-references: UNIPROT:Q99L25
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             61.4%;  Score 1469;  DB 2;  Length 446;
  Best Local Similarity   60.9%;  Pred. No. 7.4e-79;
  Matches  273;  Conservative   68;  Mismatches  103;  Indels    4;  Gaps    3;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ::|| ||| |: :|| |:||||| |||:|| |:| ||:| ||:||||:| ||||  :|:|
Db          1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120
              :  |:|: |:: | | ||||:| ||| : |:|:|:|  |  :  |  |:|| ||||| |
Db         61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSSAKT 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
                |||:|||    |:| :  |||||| |||||||::||||:|:|||||||||||  ||
Db        121 TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-LY 179

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELLGGP 238
              :||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  |||| |||||
Db        180 TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGP 238

Qy        239 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 298
              |||:|||| || |||| :| |||||||| :||:|: :|:|: |||  |:|:   | |||
Db        239 SVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNS 298

Qy        299 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 358
              | |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||  :|:
Db        299 TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEM 358

Qy        359 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 418
              || ||:|||:|  | | || ||| :||: | ||| | ||||||||:|:|||| |:|  |
Db        359 TKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWV 418

Qy        419 QGNVFSCSVMHEALHNHYTQKSLSLSPG 446
              : | :||||:|| ||||:| || | :||
Db        419 ERNSYSCSVVHEGLHNHHTTKSFSRTPG 446


RESULT 7
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>
```

```
  Query Match           61.3%;  Score 1468.5;  DB 2;  Length 469;
  Best Local Similarity  60.0%;  Pred. No. 8.3e-79;
  Matches  274;  Conservative   68;  Mismatches   98;  Indels   17;  Gaps    5;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              ::|| ||| |: ||| |:||||| |||:|| |:| ||:| ||:||:|:| |||   :|:|
Db         20 QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKPGQGLKWIGWIYPASGNTKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG--------SYWYFDLRGRGTL 112
              : :|:|: |:: | | ||||:| ||| : |||:|:|           ||     |:||
Db         80 NENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCARAMGATATLLDYW-----GQGTT 134

Qy        113 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 172
              :||||| |  |||:|||    |:| : ||||||||||||::||||:|:||||||||
Db        135 LTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPA 194

Qy        173 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CP 230
              ||||  ||:||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  ||
Db        195 VLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCP 252

Qy        231 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290
              || |||||||:|||| || |||| :| |||||||| :||:|: :|:|: |||| |:|:
Db        253 APNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 312

Qy        291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 350
              | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | ||||
Db        313 THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYV 372

Qy        351 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 410
              |||  :|:|| ||:|||:|  | | || ||| :||:  | ||| | ||||||||:|:||||
Db        373 LPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKL 432

Qy        411 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |:|  | : | :||||:|| ||||:| || | :|||
Db        433 RVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 469
```

RESULT 8
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

```
  Query Match           60.0%;  Score 1436;  DB 2;  Length 374;
  Best Local Similarity  61.7%;  Pred. No. 5.1e-77;
  Matches  280;  Conservative   29;  Mismatches   39;  Indels  106;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSF--TSYWIGWVRQMPGKGLEWMGIIYPGDSDT 58
              :: | :||  : || ::| ::|  ||:|   :  :||:|| ||: |||: :|:  | |
Db         20 QITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALEWLALIF-WDDDK 78

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC-----GSGSYWYFDLRGRGTLV 113
              ||||| : ::||: | | :   |  :::  :||| |||     | |  : |   |:||||
Db         79 RYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLV 138

Qy        114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
              ||||
Db        139 TVSS---------------------------------------------------------- 142

Qy        174 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 233
                                                  ||||||||||||||||||
Db        143 ------------------------------------------EPKSCDKTHTCPPCPAPE 160

Qy        234 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 220

Qy        294 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 280

Qy        354 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 413
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 340

Qy        414 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||
Db        341 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
```

RESULT 9
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
  Query Match           59.4%;  Score 1421;  DB 2;  Length 470;
  Best Local Similarity  60.7%;  Pred. No. 5e-76;
  Matches  276;  Conservative   58;  Mismatches  109;  Indels   12;  Gaps    6;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :||| :||  : || ::| ::|  ||:| :|| : |||| ||| |||:| |  | : | |
Db         20 QVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWVGGITSGGT-TYY 78

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYW------YFDLRGRGTLVT 114
              :|: : :::|: : | |   |  ||:   ||| |||   :|       |  |:| |||
Db         79 NPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAWGQGLLVT 138

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||  | |:||:      |  |  |||||  | ||||||:|||||| ||||||||||
```

```
Db        139 VSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYMPEPVTVTWNSGALKSGVHTFPAVL 198

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234

Db        199 QSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPPEL 255

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294

Db        256 PGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPREE 315

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354

Db        316 QFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPP 375

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 412

Db        376 QEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQLDADSSYFLYSKLRV 435

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        436 DRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK 470


RESULT 10
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

  Query Match           58.9%;  Score 1409.5;  DB 2;  Length 444;
  Best Local Similarity   58.0%;  Pred. No. 2.2e-75;
  Matches  262;  Conservative   78;  Mismatches   99;  Indels   13;  Gaps    6;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSD--T 58

Db          1 EVQXVETGGGLVRPGNSLKLSCLTSGFTFSNYRMHWLRQPPGKRLEWIAVITVKSDNYGA 60

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWY-FDLRGRGTLVTVSS 117

Db         61 KYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTPWVYAMDCWGQGTSVIVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177

Db        121 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 235

Db        181 -LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 234

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295

Db        235 --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 292

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355

Db        293 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 352

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415

Db        353 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKS 412

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        413 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444


RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

  Query Match           58.6%;  Score 1402;  DB 2;  Length 472;
  Best Local Similarity   58.5%;  Pred. No. 6.5e-75;
  Matches  269;  Conservative   64;  Mismatches  109;  Indels   18;  Gaps    5;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG---DSD 57

Db         18 QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWLG----GSGYDED 73

Qy         58 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG--------SGSYWYFDLRGR 109

Db         74 IDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWGP 133

Qy        110 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 169

Db        134 GLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVHT 193

Qy        170 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC 229

Db        194 FPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-RC 252

Qy        230 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 289

Db        253 PPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTART 312

Qy        290 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 349

Db        313 KPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQVY 372

Qy        350 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLY 407

Db        373 VLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFLY 432

Qy        408 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        433 SRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472


RESULT 12
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
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A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 1393.5; DB 2; Length 475;
Best Local Similarity 57.4%; Pred. No. 2.1e-74;
Matches 265; Conservative 71; Mismatches 105; Indels 21; Gaps 5;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              :||| |||||: :|| |:|:||| ||||: ||| | ||:|  |:||||:| ||||  :: :
Db         20 QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG--------SYWYFDLRGRGTL 112
              :  |:|: |:: ||| ||||| ||| : |:|:|:|:|              ||      |:|||
Db         80 NEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPFGYW-----GQGTL 134

Qy        113 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 172
              || |:| |  |||:|||    |:| :  |||||| |||| |||:||||:|:| ||||||
Db        135 VTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPA 194

Qy        173 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP--- 228
              :|| ||||::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||
Db        195 LLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCKE 253

Qy        229 ---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 285
                 |||| | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||
Db        254 CHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVL 313

Qy        286 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 345
              |:|:   | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  |
Db        314 TAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKIKGIVRA 373

Qy        346 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 405
              |||| | |  ::|::  ||||||  || | ||:||| |||  | ||| | |||||||:|
Db        374 PQVYILSPPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEENYKDTAPVLDSDGSYF 433

Qy        406 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              :|||| :  |:|:: : |||:| || | |:| :|::| ||||
Db        434 IYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 475
```

RESULT 13
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gam
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahas
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.9%; Score 1385; DB 1; Length 474;
Best Local Similarity 57.1%; Pred. No. 6.4e-74;
Matches 260; Conservative 74; Mismatches 113; Indels 8; Gaps 3;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
              |||| ||| |:  || |:|:||| |||:| :| : ||:| ||:||||:| | |    |::
Db         20 EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG-SYWYFDLRGRGTLVTVSSAS 119
              :  |:|: |:::||| :|||:: ||| : |:|:|||     | :|   |:||||||:|
Db         80 NEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARDYDYDWFAYWGQGTLVTVSAAK 139

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
              |  |||:||||    |:| :  ||||| |||| |||:||||:|:| |||    |  |||
Db        140 TTPPSVYPLAPGCGDTTGSSVTSGCLVKGYFPESVTVTWNSGSLSSSVHTLSQALLQSGL 199

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------CPAP 232
              |:|| ||||||:  :||  |:| |  |:| ||||:||     | : |||      ||||
Db        200 YTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAP 259

Qy        233 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 292
              | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||| |:|:
Db        260 NLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH 319

Qy        293 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 352
              | |||| |||| | : ||||::|||:||||:|| ||:|||:|||| ||  | |||| ||
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Db        320 REDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILP 379

Qy        353 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 412

Db        380 PPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM 439

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        440 KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474


RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             52.8%;  Score 1263;  DB 2;  Length 328;
  Best Local Similarity   69.6%;  Pred. No. 5.8e-67;
  Matches  231;  Conservative   43;  Mismatches   52;  Indels    6;  Gaps    2;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177

Db          1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVLQPS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237

Db         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297

Db        117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357

Db        177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 415

Db        237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

  Query Match             52.6%;  Score 1260;  DB 4;  Length 255;
  Best Local Similarity   97.5%;  Pred. No. 6.5e-67;
  Matches  233;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        209 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 268

Db         17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

Qy        269 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 328

Db         77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136

Qy        329 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 388

Db        137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy        389 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255


Search completed: September  8, 2005, 00:55:20
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:01:25 ; Search time 14.766 Seconds
(without alignments)
1086.923 Million cell updates/sec

Title: US-10-684-957-18
Perfect score: 1109
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1068.5	96.3	224	4	US-09-456-090A-52	Sequence 52, Appl
2	1068.5	96.3	224	4	US-09-453-234-52	Sequence 52, Appl
3	1066.5	96.2	226	4	US-09-456-090A-42	Sequence 42, Appl
4	1066.5	96.2	226	4	US-09-453-234-42	Sequence 42, Appl
5	1062.5	95.8	224	4	US-09-456-090A-76	Sequence 76, Appl
6	1062.5	95.8	224	4	US-09-453-234-76	Sequence 76, Appl
7	1061.5	95.7	224	4	US-09-456-090A-40	Sequence 40, Appl
8	1061.5	95.7	224	4	US-09-453-234-40	Sequence 40, Appl
9	1061	95.7	235	4	US-09-472-087-14	Sequence 14, Appl
10	1061	95.7	235	4	US-09-472-087-65	Sequence 65, Appl
11	1060.5	95.6	226	4	US-09-456-090A-38	Sequence 38, Appl
12	1060.5	95.6	226	4	US-09-453-234-38	Sequence 38, Appl
13	1059.5	95.5	224	4	US-09-456-090A-44	Sequence 44, Appl
14	1059.5	95.5	224	4	US-09-456-090A-78	Sequence 78, Appl
15	1059.5	95.5	224	4	US-09-453-234-44	Sequence 44, Appl
16	1059.5	95.5	224	4	US-09-453-234-78	Sequence 78, Appl
17	1059.5	95.5	226	4	US-09-456-090A-72	Sequence 72, Appl
18	1059.5	95.5	226	4	US-09-453-234-72	Sequence 72, Appl
19	1058.5	95.4	234	4	US-09-472-087-17	Sequence 17, Appl
20	1058.5	95.4	234	4	US-09-472-087-69	Sequence 69, Appl
21	1050.5	94.7	226	4	US-09-456-090A-86	Sequence 86, Appl
22	1050.5	94.7	226	4	US-09-453-234-86	Sequence 86, Appl
23	1047.5	94.5	226	4	US-09-456-090A-50	Sequence 50, Appl
24	1047.5	94.5	226	4	US-09-453-234-50	Sequence 50, Appl
25	1047	94.4	233	4	US-09-472-087-15	Sequence 15, Appl
26	1047	94.4	233	4	US-09-472-087-67	Sequence 67, Appl
27	1043.5	94.1	226	4	US-09-456-090A-80	Sequence 80, Appl
28	1043.5	94.1	226	4	US-09-453-234-80	Sequence 80, Appl
29	1038.5	93.6	226	4	US-09-456-090A-74	Sequence 74, Appl
30	1038.5	93.6	226	4	US-09-453-234-74	Sequence 74, Appl
31	1036.5	93.5	236	4	US-09-859-053-34	Sequence 34, Appl
32	1031.5	93.0	236	4	US-09-859-053-38	Sequence 38, Appl
33	1027.5	92.7	215	2	US-08-480-753-8	Sequence 8, Appli
34	1007	90.8	214	2	US-08-480-753-6	Sequence 6, Appli
35	1007	90.8	214	3	US-09-041-889-11	Sequence 11, Appl
36	1007	90.8	214	3	US-08-837-058-11	Sequence 11, Appl
37	1007	90.8	214	4	US-09-417-264-11	Sequence 11, Appl
38	1003.5	90.5	236	4	US-09-315-926A-79	Sequence 79, Appl
39	999.5	90.1	224	4	US-09-456-090A-82	Sequence 82, Appl
40	999.5	90.1	224	4	US-09-456-090A-88	Sequence 88, Appl
41	999.5	90.1	224	4	US-09-456-090A-90	Sequence 90, Appl
42	999.5	90.1	224	4	US-09-453-234-82	Sequence 82, Appl
43	999.5	90.1	224	4	US-09-453-234-88	Sequence 88, Appl
44	999.5	90.1	224	4	US-09-453-234-90	Sequence 90, Appl
45	998.5	90.0	224	4	US-09-456-090A-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-456-090A-52
; Sequence 52, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-25L
US-09-456-090A-52

Query Match 96.3%; Score 1068.5; DB 4; Length 224;
Best Local Similarity 98.1%; Pred. No. 4.9e-78;
Matches 210; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              :|||||||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213
```

RESULT 2
US-09-453-234-52
; Sequence 52, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars

```
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-25L
US-09-453-234-52

  Query Match             96.3%;  Score 1068.5;  DB 4;  Length 224;
  Best Local Similarity   98.1%;  Pred. No. 4.9e-78;
  Matches  210;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              :|||||||||||||||||||||||||:  |||||||||||||||||||||||||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 3
US-09-456-090A-42
; Sequence 42, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-456-090A-42

  Query Match             96.2%;  Score 1066.5;  DB 4;  Length 226;
  Best Local Similarity   97.2%;  Pred. No. 7.1e-78;
  Matches  209;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSS-FTFGPGTKVDIKRTVAAPSVFIF 119
              |||||||||||||||||||||||||||||: | |  ||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPIFTFGPGTKVDIKRTVAAPSVFIF 120

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 4
US-09-453-234-42
; Sequence 42, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-453-234-42

  Query Match             96.2%;  Score 1066.5;  DB 4;  Length 226;
  Best Local Similarity   97.2%;  Pred. No. 7.1e-78;
  Matches  209;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSS-FTFGPGTKVDIKRTVAAPSVFIF 119
              |||||||||||||||||||||||||||||: | |  ||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPIFTFGPGTKVDIKRTVAAPSVFIF 120

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 5
US-09-456-090A-76
; Sequence 76, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 76
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-16L
US-09-456-090A-76

  Query Match             95.8%;  Score 1062.5;  DB 4;  Length 224;
  Best Local Similarity   97.7%;  Pred. No. 1.5e-77;
  Matches  209;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||| |||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 DRFSVSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 6
US-09-453-234-76
; Sequence 76, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-16L
US-09-453-234-76

  Query Match             95.8%;  Score 1062.5;  DB 4;  Length 224;
  Best Local Similarity   97.7%;  Pred. No. 1.5e-77;
  Matches  209;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||| |||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 DRFSVSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 7
US-09-456-090A-40
; Sequence 40, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-4L
US-09-456-090A-40

  Query Match             95.7%;  Score 1061.5;  DB 4;  Length 224;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-77;
  Matches  209;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLHIYGASRRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQF-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 8
US-09-453-234-40
; Sequence 40, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-4L
US-09-453-234-40

  Query Match             95.7%;  Score 1061.5;  DB 4;  Length 224;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-77;
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  Matches  209;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLHIYGASRRATGIP 60

Qy         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQQF-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 9
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-14

  Query Match            95.7%;  Score 1061;  DB 4;  Length 235;
  Best Local Similarity   95.3%;  Pred. No. 2.1e-77;
  Matches  205;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||:|||:||||||:||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | | :||| |||| :|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFGQGTKVEIKRTVAAPSVFIFP 140

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 200

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||
Db        201 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 10
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-65

  Query Match            95.7%;  Score 1061;  DB 4;  Length 235;
  Best Local Similarity   95.3%;  Pred. No. 2.1e-77;
  Matches  205;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||:|||:||||||:||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | | :||| |||| :|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFGQGTKVEIKRTVAAPSVFIFP 140

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 200

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||
Db        201 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 11
US-09-456-090A-38
; Sequence 38, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-3L
US-09-456-090A-38

  Query Match            95.6%;  Score 1060.5;  DB 4;  Length 226;
  Best Local Similarity   96.7%;  Pred. No. 2.2e-77;
  Matches  208;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 12
US-09-453-234-38
; Sequence 38, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-3L
US-09-453-234-38

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  Best Local Similarity   96.7%;  Pred. No. 2.2e-77;
  Matches  208;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

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Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
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Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
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Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 13
US-09-456-090A-44
; Sequence 44, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-8L
US-09-456-090A-44

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  Matches  208;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

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Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
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RESULT 14
US-09-456-090A-78
; Sequence 78, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-18L
US-09-456-090A-78

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RESULT 15
US-09-453-234-44
; Sequence 44, Application US/09453234
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; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-8L
US-09-453-234-44

  Query Match             95.5%;  Score 1059.5;  DB 4; Length 224;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 00:14:16 ; Search time 53.5472 Seconds
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Title: US-10-684-957-18
Perfect score: 1109
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 215

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Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1109	100.0	215	17	US-10-684-957-22	Sequence 22, Appl
3	1100	99.2	215	17	US-10-684-957-20	Sequence 20, Appl
4	1072	96.7	384	15	US-10-291-265-804	Sequence 804, App
5	1072	96.7	384	15	US-10-291-265-805	Sequence 805, App
6	1072	96.7	384	15	US-10-291-265-806	Sequence 806, App
7	1072	96.7	384	15	US-10-291-265-807	Sequence 807, App
8	1069	96.4	235	17	US-10-938-353-60	Sequence 60, Appl
9	1068.5	96.3	224	10	US-09-453-234-52	Sequence 52, Appl
10	1067.5	96.3	234	15	US-10-292-088-88	Sequence 88, Appl
11	1066.5	96.2	226	10	US-09-453-234-42	Sequence 42, Appl
12	1065	96.0	215	15	US-10-307-724-122	Sequence 122, App
13	1065	96.0	215	16	US-10-737-290-122	Sequence 122, App
14	1065	96.0	235	17	US-10-938-353-32	Sequence 32, Appl
15	1065	96.0	239	16	US-10-737-290-142	Sequence 142, App
16	1062.5	95.8	224	10	US-09-453-234-76	Sequence 76, Appl
17	1062	95.8	215	18	US-10-916-758-16	Sequence 16, Appl
18	1061.5	95.7	224	10	US-09-453-234-40	Sequence 40, Appl
19	1061	95.7	235	14	US-10-153-382-7	Sequence 7, Appli
20	1061	95.7	235	16	US-10-612-497-14	Sequence 14, Appl
21	1061	95.7	235	16	US-10-612-497-65	Sequence 65, Appl
22	1061	95.7	235	16	US-10-776-649-14	Sequence 14, Appl
23	1061	95.7	235	16	US-10-776-649-65	Sequence 65, Appl
24	1061	95.7	235	17	US-10-938-353-44	Sequence 44, Appl
25	1060.5	95.6	226	10	US-09-453-234-38	Sequence 38, Appl
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27	1059.5	95.5	224	10	US-09-453-234-78	Sequence 78, Appl
28	1059.5	95.5	226	10	US-09-453-234-72	Sequence 72, Appl
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30	1058.5	95.4	234	16	US-10-612-497-17	Sequence 17, Appl
31	1058.5	95.4	234	16	US-10-612-497-69	Sequence 69, Appl
32	1058.5	95.4	234	16	US-10-776-649-17	Sequence 17, Appl
33	1058.5	95.4	234	16	US-10-776-649-69	Sequence 69, Appl
34	1053.5	95.0	234	15	US-10-292-088-72	Sequence 72, Appl
35	1050.5	94.7	226	10	US-09-453-234-86	Sequence 86, Appl
36	1049	94.6	235	15	US-10-180-648-4	Sequence 4, Appli
37	1047.5	94.5	226	10	US-09-453-234-50	Sequence 50, Appl
38	1047	94.4	233	14	US-10-153-382-11	Sequence 11, Appl
39	1047	94.4	233	16	US-10-612-497-15	Sequence 15, Appl
40	1047	94.4	233	16	US-10-612-497-67	Sequence 67, Appl
41	1047	94.4	233	16	US-10-776-649-15	Sequence 15, Appl
42	1047	94.4	233	16	US-10-776-649-67	Sequence 67, Appl
43	1043.5	94.1	226	10	US-09-453-234-80	Sequence 80, Appl
44	1041.5	93.9	216	17	US-10-684-957-33	Sequence 33, Appl
45	1038.5	93.6	226	10	US-09-453-234-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-10-684-957-18
; Sequence 18, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-18

Query Match 100.0%; Score 1109; DB 17; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
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RESULT 2
US-10-684-957-22
; Sequence 22, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-22

  Query Match             100.0%;  Score 1109;  DB 17;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-59;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-10-684-957-20
; Sequence 20, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-20

  Query Match             99.2%;  Score 1100;  DB 17;  Length 215;
  Best Local Similarity   99.5%;  Pred. No. 6.5e-59;
  Matches  214;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120

Qy         121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy         181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
               |||||||||||||||||||||||||||||||||||
Db         181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 4
US-10-291-265-804
; Sequence 804, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang et al
;  TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 804
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-804

  Query Match             96.7%;  Score 1072;  DB 15;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.3e-57;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
```

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                ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
                |||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


RESULT 5
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang et al
;  TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 805
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-805

  Query Match             96.7%;  Score 1072;  DB 15;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.3e-57;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
                ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
                |||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


RESULT 6
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang et al
;  TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 806
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-806

  Query Match             96.7%;  Score 1072;  DB 15;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.3e-57;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
                ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
                |||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 806
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-806

  Query Match             96.7%;  Score 1072;  DB 15;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.3e-57;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
                ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
                |||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


RESULT 7
US-10-291-265-807
; Sequence 807, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang et al
;  TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 807
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-807

  Query Match             96.7%;  Score 1072;  DB 15;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.3e-57;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
                ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289
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Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


RESULT 8
US-10-938-353-60
; Sequence 60, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  DEVALARAJA, MADHAV NARASIMHA
;  APPLICANT:  FOLTZ, IAN
;  APPLICANT:  HAAK-FRENDSCHO, MARY
;  APPLICANT:  KELLERMANN, SIRID-AIMEE
;  APPLICANT:  LOW, JOSEPH EDWIN
;  APPLICANT:  MOBLEY, JAMES LESLIE
;  TITLE OF INVENTION: ANTIBODIES TO M-CSF
;  FILE REFERENCE: ABX-PF4
;  CURRENT APPLICATION NUMBER: US/10/938,353
;  CURRENT FILING DATE:  2004-09-09
;  PRIOR APPLICATION NUMBER: 60/502,163
;  PRIOR FILING DATE: 2003-09-10
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 60
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-353-60

  Query Match             96.4%;  Score 1069;  DB 17;  Length 235;
  Best Local Similarity   96.7%;  Pred. No. 5.2e-57;
  Matches  208;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | |   ||| ||||:||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAPSVFIFP 140

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 200

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        201 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 9
US-09-453-234-52
; Sequence 52, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-25L
US-09-453-234-52

  Query Match             96.3%;  Score 1068.5;  DB 10;  Length 224;
  Best Local Similarity   98.1%;  Pred. No. 5.3e-57;
  Matches  210;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              :|||||||||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 10
US-10-292-088-88
; Sequence 88, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-88

  Query Match             96.3%;  Score 1067.5;  DB 15;  Length 234;
  Best Local Similarity   97.2%;  Pred. No. 6.3e-57;
  Matches  209;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSTYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||:   | ||||||||||||||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-SSLFTFGPGTKVDIKRTVAAPSVFIFP 139

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 199

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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                  ||||||||||||||||||||||||||||||||||
Db        200 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 11
US-09-453-234-42
; Sequence 42, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-453-234-42

  Query Match             96.2%;  Score 1066.5;  DB 10;  Length 226;
  Best Local Similarity   97.2%;  Pred. No. 7e-57;
  Matches  209;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSS-FTFGPGTKVDIKRTVAAPSVFIF 119
              |||||||||||||||||||||||||||||: | |  ||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPIFTFGPGTKVDIKRTVAAPSVFIF 120

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 180

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||||
Db        181 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 215


RESULT 12
US-10-307-724-122
; Sequence 122, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2cip
;  CURRENT APPLICATION NUMBER: US/10/307,724
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 134
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antibody light chain
US-10-307-724-122

  Query Match             96.0%;  Score 1065;  DB 15;  Length 215;
  Best Local Similarity   96.3%;  Pred. No. 8.3e-57;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | | :||| ||||:||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||| ||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 215


RESULT 13
US-10-737-290-122
; Sequence 122, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  APPLICANT:  Orencia, Cecilia
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2 CIP III
;  CURRENT APPLICATION NUMBER: US/10/737,290
;  CURRENT FILING DATE:  2003-12-15
;  PRIOR APPLICATION NUMBER: US 10/452,590
;  PRIOR FILING DATE: 2003-06-02
;  PRIOR APPLICATION NUMBER: US 10/307,724
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antibody light chain
US-10-737-290-122

  Query Match             96.0%;  Score 1065;  DB 16;  Length 215;
  Best Local Similarity   96.3%;  Pred. No. 8.3e-57;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
```

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              ||||||||||||||||||||||||||||||: | | :||| ||||:|||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||||||||||||||||||| ||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 215


RESULT 14
US-10-938-353-32
; Sequence 32, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  DEVALARAJA, MADHAV NARASIMHA
;  APPLICANT:  FOLTZ, IAN
;  APPLICANT:  HAAK-FRENDSCHO, MARY
;  APPLICANT:  KELLERMANN, SIRID-AIMEE
;  APPLICANT:  LOW, JOSEPH EDWIN
;  APPLICANT:  MOBLEY, JAMES LESLIE
;  TITLE OF INVENTION: ANTIBODIES TO M-CSF
;  FILE REFERENCE: ABX-PF4
;  CURRENT APPLICATION NUMBER: US/10/938,353
;  CURRENT FILING DATE:  2004-09-09
;  PRIOR APPLICATION NUMBER: 60/502,163
;  PRIOR FILING DATE: 2003-09-10
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-353-32

  Query Match             96.0%;  Score 1065;  DB 17;  Length 235;
  Best Local Similarity   96.3%;  Pred. No. 9e-57;
  Matches  207;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EFVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | |  ||| ||||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAPSVFIFP 140

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 200

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||||||||||||||||||||||||||||||||||
Db        201 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 15
US-10-737-290-142
; Sequence 142, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  APPLICANT:  Orencia, Cecilia
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2 CIP III
;  CURRENT APPLICATION NUMBER: US/10/737,290
;  CURRENT FILING DATE:  2003-12-15
;  PRIOR APPLICATION NUMBER: US 10/452,590
;  PRIOR FILING DATE: 2003-06-02
;  PRIOR APPLICATION NUMBER: US 10/307,724
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: recombinant Ab light chain
US-10-737-290-142

  Query Match             96.0%;  Score 1065;  DB 16;  Length 239;
  Best Local Similarity   96.3%;  Pred. No. 9.1e-57;
  Matches  207;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 84

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | |  ||| ||||:|||||||||||||||
Db         85 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFP 144

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 204

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||||||||||||||||||| ||||||||||
Db        205 TLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 239


Search completed: September  8, 2005, 00:48:32
Job time : 54.5472 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:11:22 ; Search time 57.9283 Seconds
(without alignments)
1435.455 Million cell updates/sec

Title: US-10-684-957-18
Perfect score: 1109
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1109	100.0	215	8	ADS87929	Ads87929 Anti-IFN-
2	1109	100.0	215	8	ADS87925	Ads87925 Anti-IFN-
3	1109	100.0	215	8	ADS94926	Ads94926 Anti-IFN-
4	1109	100.0	215	8	ADS94922	Ads94922 Anti-IFN-
5	1100	99.2	215	8	ADS87927	Ads87927 Anti-IFN-
6	1100	99.2	215	8	ADS94924	Ads94924 Anti-IFN-
7	1072	96.7	384	4	AAU14462	Aau14462 Human nov
8	1072	96.7	384	4	AAU14463	Aau14463 Human nov
9	1072	96.7	384	4	AAU14461	Aau14461 Human nov
10	1072	96.7	384	4	AAU14464	Aau14464 Human nov
11	1072	96.7	384	8	ADH80782	Adh80782 Human pol
12	1070	96.5	384	8	ADH80779	Adh80779 Human pol
13	1070	96.5	384	8	ADH80781	Adh80781 Human pol
14	1070	96.5	385	8	ADH80780	Adh80780 Human pol
15	1068.5	96.3	224	4	AAB99375	Aab99375 Human int
16	1068.5	96.3	224	4	AAB75008	Aab75008 Anti-IL8
17	1067.5	96.3	234	7	ADE28481	Ade28481 Human ant
18	1066.5	96.2	226	4	AAB99378	Aab99378 Human int
19	1066.5	96.2	226	4	AAB75011	Aab75011 Anti-IL8
20	1065	96.0	215	8	ADQ16702	Adq16702 Modified
21	1062.5	95.8	224	4	AAB99392	Aab99392 Human int
22	1062.5	95.8	224	4	AAB75025	Aab75025 Anti-IL8
23	1061.5	95.7	224	4	AAB99377	Aab99377 Human int
24	1061.5	95.7	224	4	AAB75010	Aab75010 Anti-IL8
25	1061	95.7	235	3	AAY93702	Aay93702 The kappa
26	1061	95.7	235	3	AAY93729	Aay93729 The kappa
27	1061	95.7	235	6	AAE35884	Aae35884 Human 4.1
28	1060.5	95.6	226	4	AAB99376	Aab99376 Human int
29	1060.5	95.6	226	4	AAB75009	Aab75009 Anti-IL8
30	1059.5	95.5	224	4	AAB99379	Aab99379 Human int
31	1059.5	95.5	224	4	AAB99393	Aab99393 Human int
32	1059.5	95.5	224	4	AAB75012	Aab75012 Anti-IL8
33	1059.5	95.5	224	4	AAB75026	Aab75026 Anti-IL8
34	1059.5	95.5	226	4	AAB99390	Aab99390 Human int
35	1059.5	95.5	226	4	AAB75023	Aab75023 Anti-IL8
36	1058.5	95.4	234	3	AAY93733	Aay93733 The kappa
37	1058.5	95.4	234	3	AAY93708	Aay93708 The kappa
38	1058.5	95.4	234	6	AAE35888	Aae35888 Human 6.1
39	1053.5	95.0	234	7	ADE28473	Ade28473 Human ant
40	1050.5	94.7	226	4	AAB99397	Aab99397 Human int
41	1050.5	94.7	226	4	AAB75030	Aab75030 Anti-IL8
42	1049	94.6	235	6	ABP71366	Abp71366 Anti-OPGL
43	1047.5	94.5	226	4	AAB99374	Aab99374 Human int
44	1047.5	94.5	226	4	AAB75007	Aab75007 Anti-IL8
45	1047	94.4	233	3	AAY93704	Aay93704 The kappa

ALIGNMENTS

RESULT 1
ADS87929
ID ADS87929 standard; protein; 215 AA.
XX
AC ADS87929;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 light chain SEQ ID NO:22.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 22; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36

CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1109; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-57;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 2
ADS87925
ID ADS87925 standard; protein; 215 AA.
XX
AC ADS87925;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 light chain SEQ ID NO:18.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 18; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1109; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-57;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 3
ADS94926
ID ADS94926 standard; protein; 215 AA.
XX
AC ADS94926;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 light chain SEQ ID NO:22.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX

OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 22; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1109; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-57;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 4
ADS94922
ID ADS94922 standard; protein; 215 AA.
XX
AC ADS94922;

XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 light chain SEQ ID NO:18.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 18; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1109; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-57;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
```

```
Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 5
ADS87927
ID ADS87927 standard; protein; 215 AA.
XX
AC ADS87927;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 or 1118* light chain SEQ ID NO:20.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 20; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

```
  Query Match             99.2%;  Score 1100;  DB 8;  Length 215;
  Best Local Similarity   99.5%;  Pred. No. 7.1e-57;
  Matches  214;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 6
ADS94924
ID ADS94924 standard; protein; 215 AA.
XX
AC ADS94924;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 or 1118* light chain SEQ ID NO:20.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 20; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36

CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 99.2%; Score 1100; DB 8; Length 215;
Best Local Similarity 99.5%; Pred. No. 7.1e-57;
Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 7
AAU14462
ID AAU14462 standard; protein; 384 AA.
XX
AC AAU14462;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #333.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002623.
XX
PR 25-JAN-2000; 2000US-00491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22767.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Example 4; Page 825-826; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human proteins or
CC their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides.
CC Polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/elicit an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC diseases, nervous system disorders, and infection. The present sequence
CC represents a protein of the invention
XX
SQ Sequence 384 AA;

Query Match 96.7%; Score 1072; DB 4; Length 384;
Best Local Similarity 97.2%; Pred. No. 5.1e-55;
Matches 209; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384
```

RESULT 8
AAU14463
ID AAU14463 standard; protein; 384 AA.
XX
AC AAU14463;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #334.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX

OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002623.
XX
PR 25-JAN-2000; 2000US-00491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22768.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Example 4; Page 826-827; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human proteins or
CC their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides.
CC Polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/elicit an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC diseases, nervous system disorders, and infection. The present sequence
CC represents a protein of the invention
XX
SQ Sequence 384 AA;

Query Match 96.7%; Score 1072; DB 4; Length 384;
Best Local Similarity 97.2%; Pred. No. 5.1e-55;
Matches 209; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384
```

RESULT 9
AAU14461
ID AAU14461 standard; protein; 384 AA.
XX
AC AAU14461;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #332.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002623.
XX
PR 25-JAN-2000; 2000US-00491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22766.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Example 4; Page 824-825; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human proteins or
CC their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides.
CC Polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/elicit an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC diseases, nervous system disorders, and infection. The present sequence
CC represents a protein of the invention
XX
SQ Sequence 384 AA;

Query Match 96.7%; Score 1072; DB 4; Length 384;
Best Local Similarity 97.2%; Pred. No. 5.1e-55;
Matches 209; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229
```

```
Qy          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||||
Db         230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy         121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy         181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
               |||||||||||||||||||||||||||||||||||
Db         350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384
```

RESULT 10
AAU14464
ID AAU14464 standard; protein; 384 AA.
XX
AC AAU14464;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #335.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002623.
XX
PR 25-JAN-2000; 2000US-00491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22769.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Example 4; Page 827; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human proteins or
CC their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides.
CC Polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/elicit an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC diseases, nervous system disorders, and infection. The present sequence
CC represents a protein of the invention
XX
SQ Sequence 384 AA;

```
  Query Match             96.7%;  Score 1072;  DB 4;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.1e-55;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               ||||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||||
Db         230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy         121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy         181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
               |||||||||||||||||||||||||||||||||||
Db         350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384
```

RESULT 11
ADH80782
ID ADH80782 standard; protein; 384 AA.
XX
AC ADH80782;
XX
DT 22-APR-2004 (first entry)
XX
DE Human polypeptide #99.
XX
KW Human; coagulation disorder; haemophilia; wound; stroke; thrombosis;
KW myocardial infarction; cancer; bone fracture; Alzheimer's disease;
KW Parkinson's disease; autoimmune disorder; food supplement; haemostatic;
KW vulnerary; cerebroprotective; thrombolytic; anticoagulant; cardiant;
KW cytostatic; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2003232054-A1.
XX
PD 18-DEC-2003.
XX
PF 08-NOV-2002; 2002US-00291265.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
PR 25-JAN-2001; 2001WO-US002623.
PR 03-AUG-2001; 2001US-00922279.
XX
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.

```
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Qian XB,  Wang ZW,  Wehrman T;
PI   Zhang J,  Zhou P,  Cao Y,  Drmanac RT;
XX
DR   WPI; 2004-061257/06.
XX
PT   New polynucleotides and polypeptides useful for diagnosing, preventing or
PT   treating diseases involving aberrant protein expression or activity, e.g.
PT   hemophilia, wounds, stroke, thrombosis, cancer or autoimmune disorders.
XX
PS   Claim 20; SEQ ID NO 807; 85pp; English.
XX
CC   The invention relates to new isolated polynucleotides and polypeptides.
CC   The sequences, compositions and methods of the invention are useful for
CC   diagnosing, preventing or treating diseases involving aberrant protein
CC   expression or biological activity, such as coagulation disorders (e.g.
CC   haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer,
CC   bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune
CC   disorders. The polynucleotides may be used as hybridisation probes, as
CC   oligomers or primers, for polymerase chain reaction, for chromosome and
CC   gene mapping, in the recombinant production of proteins and in generation
CC   of antisense DNA or RNA. The polypeptides may be used in generating
CC   antibodies, as molecular weight markers or as food supplements. This
CC   sequence represents a human polypeptide of the invention.
XX
SQ   Sequence 384 AA;

  Query Match             96.7%;  Score 1072;  DB 8;  Length 384;
  Best Local Similarity   97.2%;  Pred. No. 5.1e-55;
  Matches  209;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


RESULT 12
ADH80779
ID   ADH80779 standard; protein; 384 AA.
XX
AC   ADH80779;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human polypeptide #96.
XX
KW   Human; coagulation disorder; haemophilia; wound; stroke; thrombosis;
KW   myocardial infarction; cancer; bone fracture; Alzheimer's disease;
KW   Parkinson's disease; autoimmune disorder; food supplement; haemostatic;
KW   vulnerary; cerebroprotective; thrombolytic; anticoagulant; cardiant;
KW   cytostatic; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW   immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   US2003232054-A1.
XX
PD   18-DEC-2003.
XX
PF   08-NOV-2002; 2002US-00291265.
XX
PR   25-JAN-2000; 2000US-00491404.
PR   17-JUL-2000; 2000US-00617746.
PR   03-AUG-2000; 2000US-00631451.
PR   15-SEP-2000; 2000US-00663870.
PR   25-JAN-2001; 2001WO-US002623.
PR   03-AUG-2001; 2001US-00922279.
XX
PA   (TANG/) TANG Y T.
PA   (LIUC/) LIU C.
PA   (ASUN/) ASUNDI V.
PA   (CHEN/) CHEN R.
PA   (QIAN/) QIAN X B.
PA   (WANG/) WANG Z W.
PA   (WEHR/) WEHRMAN T.
PA   (ZHAN/) ZHANG J.
PA   (ZHOU/) ZHOU P.
PA   (CAOY/) CAO Y.
PA   (DRMA/) DRMANAC R T.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Qian XB,  Wang ZW,  Wehrman T;
PI   Zhang J,  Zhou P,  Cao Y,  Drmanac RT;
XX
DR   WPI; 2004-061257/06.
XX
PT   New polynucleotides and polypeptides useful for diagnosing, preventing or
PT   treating diseases involving aberrant protein expression or activity, e.g.
PT   hemophilia, wounds, stroke, thrombosis, cancer or autoimmune disorders.
XX
PS   Claim 20; SEQ ID NO 804; 85pp; English.
XX
CC   The invention relates to new isolated polynucleotides and polypeptides.
CC   The sequences, compositions and methods of the invention are useful for
CC   diagnosing, preventing or treating diseases involving aberrant protein
CC   expression or biological activity, such as coagulation disorders (e.g.
CC   haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer,
CC   bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune
CC   disorders. The polynucleotides may be used as hybridisation probes, as
CC   oligomers or primers, for polymerase chain reaction, for chromosome and
CC   gene mapping, in the recombinant production of proteins and in generation
CC   of antisense DNA or RNA. The polypeptides may be used in generating
CC   antibodies, as molecular weight markers or as food supplements. This
CC   sequence represents a human polypeptide of the invention.
XX
SQ   Sequence 384 AA;

  Query Match             96.5%;  Score 1070;  DB 8;  Length 384;
  Best Local Similarity   96.7%;  Pred. No. 6.7e-55;
  Matches  208;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              ||||||||||||||||:||||||||||||: | |  ||| ||||||||||||||||||||
Db        230 DRFSGSGSGTDFTLTISRIEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384


RESULT 13
ADH80781
ID   ADH80781 standard; protein; 384 AA.
XX
AC   ADH80781;
XX
DT   22-APR-2004  (first entry)
```

XX
DE Human polypeptide #98.
XX
KW Human; coagulation disorder; haemophilia; wound; stroke; thrombosis;
KW myocardial infarction; cancer; bone fracture; Alzheimer's disease;
KW Parkinson's disease; autoimmune disorder; food supplement; haemostatic;
KW vulnerary; cerebroprotective; thrombolytic; anticoagulant; cardiant;
KW cytostatic; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2003232054-A1.
XX
PD 18-DEC-2003.
XX
PF 08-NOV-2002; 2002US-00291265.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
PR 25-JAN-2001; 2001WO-US002623.
PR 03-AUG-2001; 2001US-00922279.
XX
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Qian XB, Wang ZW, Wehrman T;
PI Zhang J, Zhou P, Cao Y, Drmanac RT;
XX
DR WPI; 2004-061257/06.
XX
PT New polynucleotides and polypeptides useful for diagnosing, preventing or
PT treating diseases involving aberrant protein expression or activity, e.g.
PT hemophilia, wounds, stroke, thrombosis, cancer or autoimmune disorders.
XX
PS Claim 20; SEQ ID NO 806; 85pp; English.
XX
CC The invention relates to new isolated polynucleotides and polypeptides.
CC The sequences, compositions and methods of the invention are useful for
CC diagnosing, preventing or treating diseases involving aberrant protein
CC expression or biological activity, such as coagulation disorders (e.g.
CC haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer,
CC bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune
CC disorders. The polynucleotides may be used as hybridisation probes, as
CC oligomers or primers, for polymerase chain reaction, for chromosome and
CC gene mapping, in the recombinant production of proteins and in generation
CC of antisense DNA or RNA. The polypeptides may be used in generating
CC antibodies, as molecular weight markers or as food supplements. This
CC sequence represents a human polypeptide of the invention.
XX
SQ Sequence 384 AA;

Query Match 96.5%; Score 1070; DB 8; Length 384;
Best Local Similarity 96.7%; Pred. No. 6.7e-55;
Matches 208; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
Db 170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229

Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
Db 230 DRFSGSGSGTDFTLTISRIEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 289

Qy 121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
Db 290 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 349

Qy 181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
Db 350 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 384

RESULT 14
ADH80780
ID ADH80780 standard; protein; 385 AA.
XX
AC ADH80780;
XX
DT 22-APR-2004 (first entry)
XX
DE Human polypeptide #97.
XX
KW Human; coagulation disorder; haemophilia; wound; stroke; thrombosis;
KW myocardial infarction; cancer; bone fracture; Alzheimer's disease;
KW Parkinson's disease; autoimmune disorder; food supplement; haemostatic;
KW vulnerary; cerebroprotective; thrombolytic; anticoagulant; cardiant;
KW cytostatic; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2003232054-A1.
XX
PD 18-DEC-2003.
XX
PF 08-NOV-2002; 2002US-00291265.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
PR 25-JAN-2001; 2001WO-US002623.
PR 03-AUG-2001; 2001US-00922279.
XX
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
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PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Qian XB, Wang ZW, Wehrman T;
PI Zhang J, Zhou P, Cao Y, Drmanac RT;
XX
DR WPI; 2004-061257/06.
XX
PT New polynucleotides and polypeptides useful for diagnosing, preventing or
PT treating diseases involving aberrant protein expression or activity, e.g.
PT hemophilia, wounds, stroke, thrombosis, cancer or autoimmune disorders.
XX
PS Claim 20; SEQ ID NO 805; 85pp; English.
XX
CC The invention relates to new isolated polynucleotides and polypeptides.
CC The sequences, compositions and methods of the invention are useful for
CC diagnosing, preventing or treating diseases involving aberrant protein
CC expression or biological activity, such as coagulation disorders (e.g.
CC haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer,
CC bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune
CC disorders. The polynucleotides may be used as hybridisation probes, as

```
CC   oligomers or primers, for polymerase chain reaction, for chromosome and
CC   gene mapping, in the recombinant production of proteins and in generation
CC   of antisense DNA or RNA. The polypeptides may be used in generating
CC   antibodies, as molecular weight markers or as food supplements. This
CC   sequence represents a human polypeptide of the invention.
XX
SQ   Sequence 385 AA;

  Query Match             96.5%;  Score 1070;  DB 8;  Length 385;
  Best Local Similarity   96.7%;  Pred. No. 6.7e-55;
  Matches  208;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        171 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRILIYGASSRATGIP 230

Qy         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||||||||||||||||||||: | |  ||| ||||||||||||||||||||
Db        231 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVFIFP 290

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 350

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        351 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 385


RESULT 15
AAB99375
ID   AAB99375 standard; protein; 224 AA.
XX
AC   AAB99375;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Human interleukin 8 antibody protein sequence M1_25L.
XX
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033042.
XX
PR   06-DEC-1999;   99US-00456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding to
PT   nonhuman-antibodies, involves contacting sample with human antibody which
PT   binds to antibodies from nonhuman species and detecting binding.
XX
PS   Example 22; Page 94; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the amount
CC   of target antigen in a sample in a semi-quantitative or relative sense.
CC   Quantification of one or more target antigens in a sample can also be
CC   carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 224 AA;

  Query Match             96.3%;  Score 1068.5;  DB 4;  Length 224;
  Best Local Similarity   98.1%;  Pred. No. 5.1e-55;
  Matches  210;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              :|||||||||||||||||||||||||||||:  ||||||||||||||||||||||||||||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIKRTVAAPSVFIFP 119

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              |||||||||||||||||||||||||||||||||
Db        180 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


Search completed: September  8, 2005, 00:42:57
Job time : 58.9283 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:34:28 ; Search time 11.683 Seconds
(without alignments)
1770.656 Million cell updates/sec

Title: US-10-684-957-18
Perfect score: 1109
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1025	92.4	215	2	JE0242	Ig kappa chain NIG
2	989	89.2	215	2	A23746	Ig kappa chain V-I
3	966	87.1	215	2	JE0244	Ig kappa chain NIG
4	939	84.7	215	2	JE0243	Ig kappa chain NIG
5	859.5	77.5	216	2	JE0241	Ig kappa chain Am3
6	725.5	65.4	240	2	S06084	Ig kappa chain pre
7	712.5	64.2	220	2	A31790	Ig kappa chain V r
8	709	63.9	225	2	S37484	Ig kappa chain - m
9	702.5	63.3	218	2	S68241	Ig kappa chain V r
10	696.5	62.8	218	2	JC5810	monoclonal antibod
11	695	62.7	217	2	S42772	Ig kappa chain - m
12	694	62.6	219	2	S38865	Ig kappa chain - m
13	688	62.0	219	2	S52028	Ig kappa chain - m
14	688	62.0	219	2	PC4203	Ig kappa chain (mo
15	682.5	61.5	214	2	S68212	Ig kappa chain (Ma
16	679	61.2	225	2	JL0029	Ig kappa chain pre
17	678	61.1	219	2	S16112	Ig kappa chain V r
18	669	60.3	235	2	S25058	Ig kappa chain - m
19	667.5	60.2	230	2	S33161	Ig kappa chain - s
20	666.5	60.1	210	2	A56169	Ig kappa chain V r
21	665.5	60.0	234	2	S14237	Ig kappa chain pre
22	665.5	60.0	234	2	S01320	Ig kappa chain pre
23	598.5	54.0	135	2	S52059	JC-kappa protein -
24	589	53.1	178	2	PT0219	Ig kappa chain V-C
25	562	50.7	229	2	A20969	Ig kappa chain pre
26	550	49.6	238	2	A49633	Ig lambda-like cha
27	548	49.4	106	1	K3HU	Ig kappa chain C r
28	546	49.2	145	2	S20631	Ig kappa chain - h
29	543.5	49.0	144	2	PL0106	Ig kappa chain pre
30	532	48.0	197	2	S29593	Ig kappa chain (WM
31	522	47.1	109	2	H30601	Ig kappa chain V-I
32	522	47.1	109	2	B30601	Ig kappa chain V-I
33	519	46.8	109	2	A30608	Ig kappa chain V-I
34	519	46.8	109	2	C30601	Ig kappa chain V-I
35	519	46.8	109	2	D30601	Ig kappa chain V-I
36	517	46.6	109	2	G30607	Ig kappa chain V-I
37	517	46.6	129	1	K3HUHA	Ig kappa chain pre
38	517	46.6	129	1	K3HUHI	Ig kappa chain pre
39	516	46.5	107	2	PH0965	Ig kappa chain V r
40	516	46.5	129	2	S46369	IG light chain var
41	516	46.5	134	2	S38643	Ig kappa chain V r
42	515	46.4	108	2	C30608	Ig kappa chain V-I
43	515	46.4	109	2	F30607	Ig kappa chain V-I
44	513	46.3	99	2	A37927	Ig kappa chain C r
45	513	46.3	109	2	PH0963	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 1025; DB 2; Length 215;
Best Local Similarity 93.0%; Pred. No. 7.3e-61;
Matches 200; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||::|||||||||||||| |||| |||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||| |||| ||||||||||||:    :||| ||||:|||||||||||||||
Db         61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 2
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match            89.2%;  Score 989;  DB 2;  Length 215;
  Best Local Similarity   93.0%;  Pred. No. 1.7e-58;
  Matches  199;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||| |||||||||||||  |||||||:||||||||||||||||||| |||||||||
Db          1 EIVLTQSPATLSLSPGERATLSGGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||||||||||||||||||| |: | |  ||| ||||:|||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGGGTKVEIKRTVAAPSVFIFP 120

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 214
              ||||||||||||| ||||||||||||||||||
Db        181 TLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214


RESULT 3
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match            87.1%;  Score 966;  DB 2;  Length 215;
  Best Local Similarity   88.9%;  Pred. No. 5.6e-57;
  Matches  192;  Conservative    9;  Mismatches   13;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |:|||||| |||:||||||||||||||| |: |||||||||||||||| ||:||||||
Db          1 EVVLTQSPATLSVSPGERATLSCRASQSVHSN-LAWYQQKPGQAPRLLIYRASTRATGIP 59

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQR-SGGSSFTFGPGTKVDIKRTVAAPSVFIF 119
              |||||||||| |||| |: ||||:||||: :     ||| ||||:|||||||||||||
Db         60 ARFSGSGSGTDFILTISSLQSEDFALYYCQQYNTWPPLTFGGGTKVEIKRTVAAPSVFIF 119

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 4
JE0243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match            84.7%;  Score 939;  DB 2;  Length 215;
  Best Local Similarity   85.6%;  Pred. No. 3.4e-55;
  Matches  185;  Conservative   13;  Mismatches   16;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:|||| |||:|||||||||||||||::: : || || ||||||||| ||:||||:|
Db          1 EIVMTQSPATLSVSPGERATLSCRASQSVATN-VVWYMQKLGQAPRLLIYDASTRATGVP 59

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK-RTVAAPSVFIF 119
              |||||||||:|||||| |: ||||:|||| :     ||| ||||: | ||||||||||
Db         60 ARFSGSGSGTEFTLTISSLQSEDFAIYYCQHNNAWPPTFGQGTKVETKRRTVAAPSVFIF 119

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

  Query Match            77.5%;  Score 859.5;  DB 2;  Length 216;
  Best Local Similarity   78.0%;  Pred. No. 5.9e-50;
  Matches  170;  Conservative   22;  Mismatches   21;  Indels    5;  Gaps    3;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSV---SSSYLAWYQQKPGQAPRLLIYGASSRAT 57
              :|||||||  |::| |||||::|::||||    | ::|||||||| |:|||: |: | :
Db          1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ-PKLLIW-ANVRES 58

Qy         58 GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVF 117
              |:|||| ||| ||||||||| |: |  ||||||:   : ::|| | :::|||||||||||
Db         59 GVPDRFRGSGVGTDFTLTISNLQAELVAVYYCQQYYSTPYSFGQGGRLEIKRTVAAPSVF 118

Qy        118 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 178

Qy        178 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||   |||||||||||||||||||||||||||||||||
Db        179 STTLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216


RESULT 6
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
```

A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 725.5; DB 2; Length 240;
Best Local Similarity 60.9%; Pred. No. 4.4e-41;
Matches 134; Conservative 38; Mismatches 43; Indels 5; Gaps 1;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSV-----SSSYLAWYQQKPGQAPRLLIYGASSR 55
              : |:|||| :|::| ||  |::|::|||:       :||||||||||:|:|||| ||:|
Db         21 DFVMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTR 80

Qy         56 ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPS 115
              :|:|||| |||||||||||| :: || |:||| :   : :||| |||:::||  |||:
Db         81 QSGVPDRFIGSGSGTDFTLTISSVQAEDLAIYYCLQYYETPYTFGAGTKLELKRADAAPT 140

Qy        116 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 175
              | ||||| ||| :| ||||||:||||||:  |:||:|   :     :|||:|||||||||
Db        141 VSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYS 200

Qy        176 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              :||||:||||||| | :| ||| |:  |||| ||||| ||
Db        201 MSSTLSLSKADYESHNLYTCEVVHKTSSSPVVKSFNRNEC 240
```

RESULT 7
A31790
Ig kappa chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 64.2%; Score 712.5; DB 2; Length 220;
Best Local Similarity 59.5%; Pred. No. 2.9e-40;
Matches 131; Conservative 38; Mismatches 46; Indels 5; Gaps 1;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS-----YLAWYQQKPGQAPRLLIYGASSR 55
              :||:|||| :|::: ||: |:|| :|||: :|     || |||||||| |::||| ||:|
Db          1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTR 60

Qy         56 ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPS 115
              :|:||||:|||||||||||| :: || ||||||     :  ||| |||:::||  |||:
Db         61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLELKRADAAPT 120

Qy        116 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 175
              | ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||||
Db        121 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 180

Qy        176 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              :||||||:| :||:|  | || ||:  :||: ||||| ||
Db        181 MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 220
```

RESULT 8
S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 63.9%; Score 709; DB 2; Length 225;
Best Local Similarity 63.1%; Pred. No. 5e-40;
Matches 135; Conservative 34; Mismatches 43; Indels 2; Gaps 2;

```
Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD 61
              ||:||:|  | || |:| |::|:|||||:  :|||||||||:|:|||| |||| ||:||
Db         14 IVMTQTPKFLLLSAGDRVTITCKASQSVSND-VAWYQQKPGQSPKLLIYYASSRYTGVPD 72

Qy         62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFPP 121
              ||:||| ||||| ||| :: || |||:||:   ||:||| |||::|||  |||:| ||||
Db         73 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQD-YSSYTFGGGTKLEIKRADAAPTVSIFPP 131

Qy        122 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 181
              | ||| || ||||| ||||||::  |:||:| : :      | |:|||||||:|||||
Db        132 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 191

Qy        182 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |:| :||:|  | || ||:  :||: ||||| ||
Db        192 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 225
```

RESULT 9
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyri
A;Reference number: S68241
A;Accession: S68241
A;Molecule type: mRNA
A;Residues: 1-218 <TAK>
A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68214
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'NI',3-212 <TAW>
A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Query Match 63.3%; Score 702.5; DB 2; Length 218;
Best Local Similarity 61.5%; Pred. No. 1.3e-39;
Matches 134; Conservative 33; Mismatches 48; Indels 3; Gaps 1;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS---YLAWYQQKPGQAPRLLIYGASSRAT 57
              |:|||||| :|::| |:|||:|||||:|||:|   |: ||||||| |:|||  |::  :
Db          1 ELVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLATNLES 60

Qy         58 GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVF 117
              |:| |||||||||||| |  :| || | |||| |     ||| |||:::||  |||:|
Db         61 GVPARFSGSGSGTDFTLNIHPVEEEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVS 120
```

```
Qy        118 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177
              ||||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||:|
Db        121 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 180

Qy        178 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||:| :||:|  | || ||:  :||: ||||||||
Db        181 STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 218


RESULT 10
JC5810
monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: JC5810
R;Akashi, S.; Kato, K.; Tórizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: JC5810
A;Molecule type: protein
A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>

  Query Match             62.8%;  Score 696.5;  DB 2;  Length 218;
  Best Local Similarity   61.8%;  Pred. No. 3.2e-39;
  Matches  134;  Conservative   31;  Mismatches   49;  Indels    3;  Gaps    1;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSVSSS---YLAWYQQKPGQAPRLLIYGASSRATG 58
              ||||||| :|::| |:|||:|||||:|||:|   |: |||||||| |:||| ||:  :|
Db          2 IVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLASNLESG 61

Qy         59 IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFI 118
              :| |||||||||||| |  :| || | |||| |     ||| |||:::||  |||:| |
Db         62 VPARFSGSGSGTDFTLNIHPVEEEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVSI 121

Qy        119 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 178
              |||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||:||
Db        122 FPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS 181

Qy        179 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||:| :||:|  | || ||:  :||: ||||| ||
Db        182 TLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 218


RESULT 11
S42772
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42772
R;Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42771
A;Accession: S42772
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <SCH>
A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-93/Domain: immunoglobulin homology <IMM>

  Query Match             62.7%;  Score 695;  DB 2;  Length 217;
  Best Local Similarity   59.9%;  Pred. No. 4e-39;
  Matches  130;  Conservative   37;  Mismatches   46;  Indels    4;  Gaps    1;

Qy          3 VLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSRATG 58
              |:|||| :| :| |::|::|||:|||:     ::|| || ||||||:|::|||  |:| :|
Db          1 VMTQSPLSLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGQSPKVLIYKVSTRFSG 60

Qy         59 IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFI 118
              :|||||||||||||  |||:| ||  ||:| :|    |||| |||::|||  |||:| |
Db         61 VPDRFSGSGSGTDFTFKISRVEAEDLGVYFCSQSTYVPFTFGSGTKLEIKRADAAPTVSI 120

Qy        119 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 178
              |||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||:||
Db        121 FPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS 180

Qy        179 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||:| :||:|  | || ||:  :||: ||||| ||
Db        181 TLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 217


RESULT 12
S38865
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of an
A;Reference number: S38864
A;Accession: S38865
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <KIP>
A;Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             62.6%;  Score 694;  DB 2;  Length 219;
  Best Local Similarity   59.8%;  Pred. No. 4.7e-39;
  Matches  131;  Conservative   38;  Mismatches   46;  Indels    4;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSRA 56
              |:|:|||| :||:| |::|::|||:|||:     ::|| || |||| :|:||||  |:|
Db          1 ELVMTQSPLSLSVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGLSPKLLIYIVSNRF 60

Qy         57 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSV 116
              :|:|||||||||||||| |||:| ||  ||:| :     :||| |||::|||  |||:|
Db         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQVTHVPWTFGGGTKLEIKRADAAPTV 120

Qy        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176
               ||||| ||| || ||||| ||||||::  |:||:| : :      | |:||||||||:
Db        121 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 180

Qy        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||||:| :||:|  | || ||:  :||: ||||||||
Db        181 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 219


RESULT 13
S52028
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun
A;Reference number: S52028
A;Accession: S52028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

  Query Match             62.0%;  Score 688;  DB 2;  Length 219;
  Best Local Similarity   58.9%;  Pred. No. 1.2e-38;
```

```
  Matches  129;  Conservative   37;  Mismatches   49;  Indels    4;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSRA 56
              ::|:|||| :| :| |::|::|||:|||:     ::|| || |||||:|:|||| |:|
Db          1 DVVMTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60

Qy         57 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSV 116
              :|:|||||||||||||| |||:| ||  |||| :      ||| || ::|||  |||:|
Db         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTNLEIKRADAAPTV 120

Qy        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176
               ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||||:
Db        121 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 180

Qy        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||||:| :||:|  | || ||:  :||: ||||| ||
Db        181 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219


RESULT 14
PC4203
Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mo
A;Reference number: PC4202; MUID:97082978; PMID:8964510
A;Accession: PC4203
A;Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

  Query Match           62.0%;  Score 688;  DB 2;  Length 219;
  Best Local Similarity   58.4%;  Pred. No. 1.2e-38;
  Matches  128;  Conservative   39;  Mismatches   48;  Indels    4;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSRA 56
              ::::||:| :| :| |::|::|||:|||:     ::|| || |||||:|:|||| |:|
Db          1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHTNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60

Qy         57 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSV 116
              :|:|||||||||||||| |||:| ||  |||| :      ||| |||::|||  |||:|
Db         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPRTFGGGTKLEIKRADAAPTV 120

Qy        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176
               ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||||:
Db        121 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 180

Qy        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              ||||||:| :||:|  | || ||:  :||: |||||  ||
Db        181 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219


RESULT 15
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68212
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68212
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-214 <TAK>
A;Cross-references: EMBL:D29668
C;Superfamily: immunoglobulin V region; immunoglobulin homology

  Query Match           61.5%;  Score 682.5;  DB 2;  Length 214;
  Best Local Similarity   58.9%;  Pred. No. 2.6e-38;
  Matches  126;  Conservative   41;  Mismatches   42;  Indels    5;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS-----YLAWYQQKPGQAPRLLIYGASSR 55
              :||:|||| :|::| |:: |:||::|||: :|     |||||||||||:|:||:| ||:|
Db          1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQSPKLLVYFASTR 60

Qy         56 ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPS 115
               :|:|||| |||||||||||||| :: || | |:||:   : :||| |||::|||  |||:
Db         61 ESGVPDRFIGSGSGTDFTLTISTVQAEDLADYFCQQHYSTPYTFGGGTKLEIKRADAAPT 120

Qy        116 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 175
               | ||||| ||| || ||||| ||||||::  |:||:| : :      | |:|||||||||
Db        121 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 180

Qy        176 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS 209
              :||||||:| :||:|  | || ||:  :||: ||
Db        181 MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS 214


Search completed: September  8, 2005, 00:55:19
Job time : 13.683 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:15:52 ; Search time 52.2491 Seconds
(without alignments)
2107.158 Million cell updates/sec

Title: US-10-684-957-18
Perfect score: 1109
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....EVTHQGLSSPVTKSFNRGEC 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1055	95.1	235	2	Q6PJF2	Q6pjf2 homo sapien
2	1041.5	93.9	236	2	Q6PIL8	Q6pil8 homo sapien
3	1030.5	92.9	236	2	Q6P5S8	Q6p5s8 homo sapien
4	1025	92.4	235	2	Q6GMV9	Q6gmv9 homo sapien
5	968	87.3	235	2	Q6GMW0	Q6gmw0 homo sapien
6	953.5	86.0	236	2	Q6GMX8	Q6gmx8 homo sapien
7	933.5	84.2	236	2	Q6PIH7	Q6pih7 homo sapien
8	919.5	82.9	236	2	Q6GMW1	Q6gmw1 homo sapien
9	914.5	82.5	236	2	Q6GMX0	Q6gmx0 homo sapien
10	912.5	82.3	236	2	Q7Z3Y4	Q7z3y4 homo sapien
11	911.5	82.2	236	2	Q6PIH4	Q6pih4 homo sapien
12	908.5	81.9	234	2	Q7Z473	Q7z473 homo sapien
13	907.5	81.8	236	2	Q6GMX9	Q6gmx9 homo sapien
14	906.5	81.7	236	2	Q6PIT5	Q6pit5 homo sapien
15	899	81.1	239	2	Q8NEK0	Q8nek0 homo sapien
16	898.5	81.0	240	2	Q6PIH6	Q6pih6 homo sapien
17	874	78.8	239	2	Q8TCD0	Q8tcd0 homo sapien
18	867	78.2	239	2	Q6P491	Q6p491 homo sapien
19	699.5	63.1	238	2	Q66JS7	Q66js7 mus musculu
20	696	62.8	219	2	Q65ZC0	Q65zc0 mus musculu
21	659.5	59.5	236	2	Q7TS98	Q7ts98 mus musculu
22	642.5	57.9	241	2	Q63ZX4	Q63zx4 mus musculu
23	595.5	53.7	237	2	Q7SZ36	Q7sz36 xenopus lae
24	591	53.3	120	2	Q6P5R5	Q6p5r5 homo sapien
25	587	52.9	243	2	Q6NTU5	Q6ntu5 xenopus lae
26	548	49.4	106	1	KAC_HUMAN	P01834 homo sapien
27	521	47.0	109	2	Q9UL86	Q9ul86 homo sapien
28	517	46.6	129	1	KV3L_HUMAN	P18135 homo sapien
29	517	46.6	129	1	KV3M_HUMAN	P18136 homo sapien
30	513	46.3	109	2	Q9UL78	Q9ul78 homo sapien
31	509	45.9	109	1	KV3B_HUMAN	P01620 homo sapien
32	506	45.6	109	1	KV3E_HUMAN	P01623 homo sapien
33	502	45.3	109	1	KV3D_HUMAN	P01622 homo sapien
34	484	43.6	108	1	KV3A_HUMAN	P01619 homo sapien
35	481	43.4	109	1	KV3G_HUMAN	P04206 homo sapien
36	462	41.7	100	1	KV3C_HUMAN	P01621 homo sapien
37	462	41.7	233	2	Q8TBC9	Q8tbc9 homo sapien
38	460.5	41.5	236	2	Q6GMX4	Q6gmx4 homo sapien
39	458	41.3	235	2	Q6IN99	Q6in99 homo sapien
40	455.5	41.1	236	2	Q8NEJ1	Q8nej1 homo sapien
41	450.5	40.6	108	2	Q9UL83	Q9ul83 homo sapien
42	448.5	40.4	128	1	KV3K_HUMAN	P06311 homo sapien
43	448.5	40.4	234	2	Q6GMW3	Q6gmw3 homo sapien
44	447.5	40.4	234	2	Q8N355	Q8n355 homo sapien
45	445.5	40.2	234	2	Q7Z2U7	Q7z2u7 homo sapien

ALIGNMENTS

RESULT 1
Q6PJF2
ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

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KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match           95.1%;  Score 1055;  DB 2;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 3e-80;
  Matches  204;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||| |||||||||||||||| |||:|||||||||||||||::|:||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||||||||||||||||||||: | |  ||||||||||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDIKRTVAAPSVFIFP 140

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 200

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        201 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 2
Q6PIL8
ID   Q6PIL8      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032451; AAH32451.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match           93.9%;  Score 1041.5;  DB 2;  Length 236;
  Best Local Similarity   94.4%;  Pred. No. 4e-79;
  Matches  204;  Conservative    4;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              | |||||||||||||||||||||||:|||||||||||||||||||| ||||||||
Db         21 ENVLTQSPGTLSLSPGERATLSCRASQSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIKRTVAAPSVFIF 119
              ||||||||||||||||||||||||||||||: | |   ||| ||::|||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDIKRTVAAPSVFIF 140

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 3
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match             92.9%;  Score 1030.5;  DB 2;  Length 236;
  Best Local Similarity   93.1%;  Pred. No. 3.4e-78;
  Matches  201;  Conservative    8;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||| ||||||||||||||:| ||:||||||:||||||||||||||||||||
Db         21 EIVLTQSPGTLSFSPGERATLSCRASQTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIKRTVAAPSVFIF 119
              |||||||||||||||:||||||||||:||: | | | ||| ||:|:|||||||||||||
Db         81 DRFSGSGSGSGTDFTLTITRLEPEDFAVYFCQQYGTSPSLTFGGGTRVEIKRTVAAPSVFIF 140

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 200

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 4
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             92.4%;  Score 1025;  DB 2;  Length 235;
  Best Local Similarity   92.6%;  Pred. No. 9.7e-78;
  Matches  199;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||| |||||||||:| ||||||||||||||:| || ||||||
Db         21 EIVLTQSPGTLSLSPGERAALSCRASQSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||||||||||| ||||:|:||: | |  ||| ||||:|||||||||||||||
Db         81 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGTSPLTFGGGTKVEIKRTVAAPSVFIFP 140

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 200

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        201 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 5
Q6GMW0
ID   Q6GMW0      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMW0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
```

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RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073792; AAH73792.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25765 MW;  4360C36B6D4133F5 CRC64;

  Query Match             87.3%;  Score 968;  DB 2;  Length 235;
  Best Local Similarity   87.5%;  Pred. No. 5.7e-73;
  Matches  189;  Conservative   15;  Mismatches   10;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:|||| |||:|||||||||||||||:|:: ||||||:|||||||||||||| ||||
Db         21 EIVMTQSPATLSVSPGERATLSCRASQSISNN-LAWYQQRPGQAPRLLIYGASSRVTGIP 79

Qy         61 DRFSGSGSGSGTDFTLTISRLEPEDFAVYYCQR-SGGSSFTFGPGTKVDIKRTVAAPSVFIF 119
              |||||||||:|||:|| |: |||||:||: :    :||| ||||::||||||||||||
Db         80 GRFSGSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWLLYTFGQGTKLEIKRTVAAPSVFIF 139

Qy        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 6
Q6GMX8
ID   Q6GMX8      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match             86.0%;  Score 953.5;  DB 2;  Length 236;
  Best Local Similarity   84.7%;  Pred. No. 9.3e-72;
  Matches  182;  Conservative   16;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :| :|||| ::| | |:| |::||||| : ||:||||||||:||:|||| |||  :|:|
Db         23 DIQMTQSPSSVSASVGDRVTITCRASQGI-SSWLAWYQQKPGKAPKLLIYAASSLQSGVP 81

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               |||||||||||||| |:||||| ||||::    |||||||||||||||||||||||
Db         82 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFPFTFGPGTKVDIKRTVAAPSVFIFP 141

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 7
Q6PIH7
ID   Q6PIH7      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25603 MW;  8BC561106861213F CRC64;

  Query Match             84.2%;  Score 933.5;  DB 2;  Length 236;
  Best Local Similarity   84.2%;  Pred. No. 4.4e-70;
  Matches  181;  Conservative   13;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :| |||||  || | |:| |::||||| : |||||||||||||:|| |||| ||:  :|:|
Db         23 DIQLTQSPSFLSASVGDRVTITCRASQGI-SSYLAWYQQKPGKAPNLLIYAASTLQSGVP 81

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
              |||||||||:|||||| |:||||| ||||:    |  ||| ||||:|||||||||||||
Db         82 SRFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSSPPTFGGGTKVEIKRTVAAPSVFIFP 141

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 8
Q6GMW1
ID   Q6GMW1      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             82.9%;  Score 919.5;  DB 2;  Length 236;
  Best Local Similarity   82.7%;  Pred. No. 6.5e-69;
  Matches  177;  Conservative   15;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD 61
              | :|||| :|| | |:| |::||||| :|:  | |||||||:||:|||| |||  :|:|
Db         24 IQMTQSPSSLSASVGDRVTITCRASQGISND-LGWYQQKPGKAPKLLIYAASSLQSGVPS 82

Qy         62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFPP 121
              |||||||||||||| |:||||| ||| :     :||| ||||:||||||||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEIKRTVAAPSVFIFPP 142

Qy        122 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 202

Qy        182 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||
Db        203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 9
Q6GMX0
ID   Q6GMX0      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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```
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073775; AAH73775.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25807 MW;  864EA08C7E92BF8F CRC64;

  Query Match             82.5%;  Score 914.5;  DB 2;  Length 236;
  Best Local Similarity   81.9%;  Pred. No. 1.7e-68;
  Matches  176;  Conservative   16;  Mismatches   22;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :| :|||| :|| | |:| |::||||:: ::|| ||| |||:|| |||| ||| :|:|
Db         23 DIQMTQSPSSLSASVGDRVTITCRASQNI-NNYLNWYQLKPGKAPNLLIYAASSLQSGVP 81

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               |||||||||||||||| | |:||| ||||:|     ||| || |:||||||||||||||
Db         82 SRFSGSGSGTDFTLTISSLRPDDFATYYCQQSYNIPLTFGGGTNVEIKRTVAAPSVFIFP 141

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 10
Q7Z3Y4
ID   Q7Z3Y4      PRELIMINARY;      PRT;   236 AA.
AC   Q7Z3Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25702 MW;  7FBFE4ED23084BC6 CRC64;

  Query Match             82.3%;  Score 912.5;  DB 2;  Length 236;
  Best Local Similarity   81.4%;  Pred. No. 2.5e-68;
  Matches  175;  Conservative   18;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :| :|||| :|| | |:  |::||||| : |:||||:||||:||: |||||||  :|:
Db         23 DIQMTQSPSSLSASVGDTVTITCRASQDI-SNYLAWFQQKPGKAPKSLIYGASSLQSGVQ 81

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               :|||||||||||||| |:||||| ||||:       ||| |||::||||||||||||||
Db         82 SKFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIKRTVAAPSVFIFP 141

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 11
Q6PIH4
ID   Q6PIH4      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034146; AAH34146.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25871 MW;  BE01A28CD06EEE26 CRC64;

  Query Match             82.2%;  Score 911.5;  DB 2;  Length 236;
  Best Local Similarity   81.9%;  Pred. No. 3.1e-68;
  Matches  176;  Conservative   17;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :| :|||| ||| | |:| |::||||| : | :|||||||||:||:|||| ||   :|:|
Db         23 DIQMTQSPSTLSASVGDRVTIACRASQWI-SDWLAWYQQKPGKAPKLLIYDASRLESGVP 81

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               |||||||||:|:|||| |:|:||| ||||    :|  || ||||:||||||||||||||
Db         82 SRFSGSGSGTEFSLTISGLQPDDFATYYCQPYNSNSPQFGQGTKVEIKRTVAAPSVFIFP 141

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 12
Q7Z473
ID   Q7Z473      PRELIMINARY;      PRT;   234 AA.
AC   Q7Z473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

  Query Match             81.9%;  Score 908.5;  DB 2;  Length 234;
  Best Local Similarity   82.2%;  Pred. No. 5.4e-68;
  Matches  176;  Conservative   16;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD 61
              | :|||| : | | |:| |::||||||:  ||||||||||:||:|||| ||:  :|:|
Db         22 IRMTQSPSSFSASTGDRVTITCRASQSI-GSYLAWYQQKPGKAPQLLIYAASTLQSGVPS 80

Qy         62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFPP 121
              ||||| |||||||:|| |: |||| ||||:     :||| ||||:|||||||||||||||
Db         81 RFSGSASGTDFTLSISCLQSEDFATYYCQQYYTYPWTFGQGTKVEIKRTVAAPSVFIFPP 140

Qy        122 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 200

Qy        182 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||
Db        201 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
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RESULT 13
Q6GMX9
ID   Q6GMX9      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073763; AAH73763.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25924 MW;  FDE2093DC560CFF7 CRC64;

  Query Match           81.8%;  Score 907.5;  DB 2;  Length 236;
  Best Local Similarity   81.9%;  Pred. No. 6.6e-68;
  Matches  176;  Conservative   15;  Mismatches   23;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :| :|||| :|| | | | |::|||||:| | :||||||:| :||: |||  ||   :|:|
Db         23 DIQMTQSPSSLSASVGHRVTITCRASQNV-SRWLAWYQQRPEKAPKSLIYATSSLHSGVP 81

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFP 120
               |||||||||||||| |:||||| ||||:       ||| ||||:|||||||||||||
Db         82 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEIKRTVAAPSVFIFP 141

Qy        121 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        181 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 14
Q6PIT5
ID   Q6PIT5      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIT5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029444; AAH29444.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25741 MW;  BD50AF071FEEE351 CRC64;

  Query Match           81.7%;  Score 906.5;  DB 2;  Length 236;
  Best Local Similarity   82.2%;  Pred. No. 8e-68;
  Matches  176;  Conservative   15;  Mismatches   22;  Indels    1;  Gaps    1;

Qy          2 IVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD 61
              | ||||| :|| | ||| |::||||| :||: |||||||||: |:|||| ||:  :|:|
Db         24 IQLTQSPSSLSASVGERVTITCRASQGISSA-LAWYQQKPGKPPKLLIYDASTMESGVPS 82

Qy         62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSVFIFPP 121
              ||||||||| |||||| |:||||| :|||:       ||| || ::|||||||||||||
Db         83 RFSGSGSGTHFTLTISSLQPEDFATFYCQQFKSYPRTFGQGTTLEIKRTVAAPSVFIFPP 142
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Qy        122 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 202

Qy        182 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||
Db        203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 15
Q8NEK0
ID   Q8NEK0      PRELIMINARY;      PRT;   239 AA.
AC   Q8NEK0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030814; AAH30814.1; -.
DR   PIR; S23638; S23638.
DR   PIR; S34091; S34091.
DR   PIR; S40342; S40342.
DR   PIR; S40357; S40357.
DR   HSSP; P01834; 1I7Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   239 AA;  26024 MW;  F5E20AD3B0552C0A CRC64;

  Query Match             81.1%;  Score 899;  DB 2;  Length 239;
  Best Local Similarity   79.5%;  Pred. No. 3.4e-67;
  Matches  174;  Conservative   20;  Mismatches   21;  Indels    4;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS----YLAWYQQKPGQAPRLLIYGASSRA 56
              :||:|||| :| ::||| |::|||:|||:  |    || || |||||:|:||||  |:||
Db         21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA 80

Qy         57 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIKRTVAAPSV 116
              :|:|||||||||||||| ||::| ||  :||| :   :  ||| ||||:||||||||||
Db         81 SGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTPQTFGQGTKVEIKRTVAAPSV 140

Qy        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNTLQSGNSQESVTEQDSKDSTYSL 200

Qy        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
              |||||||||||||||||||||||||||||||||||||||
Db        201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239


Search completed: September  8, 2005, 00:54:02
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:14:16 ; Search time 111.328 Seconds
(without alignments)
1581.260 Million cell updates/sec

Title: US-10-684-957-17
Perfect score: 2390
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2390	100.0	447	17	US-10-684-957-17	Sequence 17, Appl
2	2379	99.5	447	17	US-10-684-957-21	Sequence 21, Appl
3	2374	99.3	447	17	US-10-684-957-19	Sequence 19, Appl
4	2360	98.7	447	17	US-10-684-957-32	Sequence 32, Appl
5	2286.5	95.7	468	16	US-10-769-144-2	Sequence 2, Appli
6	2286.5	95.7	468	18	US-10-903-191-2	Sequence 2, Appli
7	2286.5	95.7	613	16	US-10-769-144-10	Sequence 10, Appl
8	2286.5	95.7	613	18	US-10-903-191-10	Sequence 10, Appl
9	2273	95.1	474	15	US-10-291-265-284	Sequence 284, App
10	2258.5	94.5	467	15	US-10-656-769-32	Sequence 32, Appl
11	2218	92.8	451	17	US-10-849-615-69	Sequence 69, Appl
12	2164	90.5	470	14	US-10-216-484-157	Sequence 157, App
13	2164	90.5	470	14	US-10-384-933-157	Sequence 157, App
14	2160	90.4	470	14	US-10-216-484-147	Sequence 147, App
15	2160	90.4	470	14	US-10-384-933-147	Sequence 147, App
16	2159.5	90.4	731	9	US-09-825-012-46	Sequence 46, Appl
17	2159.5	90.4	741	9	US-09-825-012-55	Sequence 55, Appl
18	2159	90.3	470	14	US-10-216-484-145	Sequence 145, App
19	2159	90.3	470	14	US-10-384-933-145	Sequence 145, App
20	2157	90.3	448	15	US-10-411-037-56	Sequence 56, Appl
21	2157	90.3	448	15	US-10-411-026-56	Sequence 56, Appl
22	2157	90.3	448	15	US-10-410-962-56	Sequence 56, Appl
23	2157	90.3	448	15	US-10-411-049-56	Sequence 56, Appl
24	2157	90.3	448	16	US-10-410-930-56	Sequence 56, Appl
25	2157	90.3	448	16	US-10-410-997-56	Sequence 56, Appl
26	2157	90.3	448	16	US-10-411-012-56	Sequence 56, Appl
27	2157	90.3	448	16	US-10-287-994-56	Sequence 56, Appl
28	2157	90.3	448	16	US-10-410-913-56	Sequence 56, Appl
29	2157	90.3	448	17	US-10-410-980-56	Sequence 56, Appl
30	2157	90.3	448	17	US-10-410-897-56	Sequence 56, Appl
31	2157	90.3	448	17	US-10-492-261-56	Sequence 56, Appl
32	2157	90.3	451	15	US-10-423-299-4	Sequence 4, Appli
33	2157	90.3	470	14	US-10-216-484-143	Sequence 143, App
34	2157	90.3	470	14	US-10-384-933-143	Sequence 143, App
35	2156	90.2	470	14	US-10-216-484-117	Sequence 117, App
36	2156	90.2	470	14	US-10-384-933-117	Sequence 117, App
37	2154.5	90.1	452	16	US-10-818-765-4	Sequence 4, Appli
38	2154.5	90.1	452	17	US-10-861-049-16	Sequence 16, Appl
39	2154.5	90.1	452	20	US-11-021-874-16	Sequence 16, Appl
40	2154.5	90.1	452	20	US-11-005-677-4	Sequence 4, Appli
41	2154.5	90.1	471	17	US-10-877-363-4	Sequence 4, Appli
42	2154.5	90.1	471	17	US-10-922-651-4	Sequence 4, Appli
43	2154.5	90.1	471	17	US-10-861-049-4	Sequence 4, Appli
44	2154.5	90.1	471	20	US-11-021-874-4	Sequence 4, Appli
45	2154.5	90.1	729	9	US-09-825-012-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-10-684-957-17
; Sequence 17, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 447
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-684-957-17

Query Match 100.0%; Score 2390; DB 17; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

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Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120

Qy         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 2
US-10-684-957-21
; Sequence 21, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-21

Query Match 99.5%; Score 2379; DB 17; Length 447;
Best Local Similarity 99.6%; Pred. No. 1.6e-151;
Matches 445; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
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Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db         421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 3
US-10-684-957-19
; Sequence 19, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-19

Query Match 99.3%; Score 2374; DB 17; Length 447;
Best Local Similarity 99.3%; Pred. No. 3.5e-151;
Matches 444; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
               ||||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||||
Db           1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120
               ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy         301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
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Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
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Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 4
US-10-684-957-32
; Sequence 32, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-32

  Query Match             98.7%;  Score 2360;  DB 17;  Length 447;
  Best Local Similarity   99.1%;  Pred. No. 3e-150;
  Matches  443;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                ||||||||||||||||||||||||||||||||||||||||:|||| ||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
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Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
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Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
                ||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 5
US-10-769-144-2
; Sequence 2, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Endres, Michael
;  APPLICANT:  He, Lizhen
;  APPLICANT:  Ramakrishna, Venky
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301
;  CURRENT APPLICATION NUMBER: US/10/769,144
;  CURRENT FILING DATE:  2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 468
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-769-144-2

  Query Match             95.7%;  Score 2286.5;  DB 16;  Length 468;
  Best Local Similarity   96.6%;  Pred. No. 2.7e-145;
  Matches  432;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
                ||||||||||||||||||:|||||||| :||:|||||||||||||||| |||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                |||||||||||||||||||||||||||||||||||  |     | ||:||||||||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDR-GVDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
                ||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 6
US-10-903-191-2
; Sequence 2, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Endres, Michael
;  APPLICANT:  He, Lizhen
;  APPLICANT:  Ramakrishna, Venky
```

```
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301CP
;  CURRENT APPLICATION NUMBER: US/10/903,191
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 10/769144
;  PRIOR FILING DATE: 2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 468
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-903-191-2

  Query Match             95.7%;  Score 2286.5;  DB 18;  Length 468;
  Best Local Similarity   96.6%;  Pred. No. 2.7e-145;
  Matches  432;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||| :||:||||||||||||| |||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||| |      | ||:|||||||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDR-GVDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 7
US-10-769-144-10
; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Endres, Michael
;  APPLICANT:  He, Lizhen
;  APPLICANT:  Ramakrishna, Venky
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301
;  CURRENT APPLICATION NUMBER: US/10/769,144
;  CURRENT FILING DATE:  2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-769-144-10

  Query Match             95.7%;  Score 2286.5;  DB 16;  Length 613;
  Best Local Similarity   96.6%;  Pred. No. 3.7e-145;
  Matches  432;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||| :||:||||||||||||| |||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||| |      | ||:|||||||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDR-GVDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 8
US-10-903-191-10
; Sequence 10, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Endres, Michael
;  APPLICANT:  He, Lizhen
;  APPLICANT:  Ramakrishna, Venky
;  TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: MXI-301CP
;  CURRENT APPLICATION NUMBER: US/10/903,191
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: 10/769144
;  PRIOR FILING DATE: 2004-01-30
;  PRIOR APPLICATION NUMBER: 60/443979
;  PRIOR FILING DATE: 2003-01-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-903-191-10

  Query Match             95.7%;  Score 2286.5;  DB 18;  Length 613;
  Best Local Similarity   96.6%;  Pred. No. 3.7e-145;
  Matches  432;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
```

```
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDR-GVDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465
```

RESULT 9
US-10-291-265-284
; Sequence 284, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 284
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-284

Query Match 95.1%; Score 2273; DB 15; Length 474;
Best Local Similarity 93.8%; Pred. No. 2.2e-144;
Matches 427; Conservative 9; Mismatches 11; Indels 8; Gaps 2;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
Db         20 EVQLVQSGAEVKKPGESVKISCKGSGYSFSDYWVAWVRQSPDKGLAWMGIIYPGDSDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG------SYFYF--DLWGRGTL 112
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKDSDTAMYYCARGARGTAPSYHYYGLDVWGRGTS 139

Qy        113 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 172
```

```
Db        140 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199

Qy        173 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 232
Db        200 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259

Qy        233 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 292
Db        260 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 319

Qy        293 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 352
Db        320 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 379

Qy        353 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 412
Db        380 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 439

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
Db        440 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
```

RESULT 10
US-10-656-769-32
; Sequence 32, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-32

Query Match 94.5%; Score 2258.5; DB 15; Length 467;
Best Local Similarity 94.9%; Pred. No. 2.1e-143;
Matches 425; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
Db         20 EVQLMQSGAEVKKPGESLKISCKGSGYSFSFHWIAWVRQMPGKGLEWMGIIHPGASDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFYFDLWGRGTLVTVSSAS 119
Db         80 SPSFQGQVTISADNSNSATYLQWSSLKASDTAMYFCARQRELDYFDYWGQGTLVTVSSAS 139

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
Db        140 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 199

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 239
Db        200 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 259

Qy        240 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 299
Db        260 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 319

Qy        300 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 359
Db        320 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 379
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Qy        360 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 439

Qy        420 GNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||
Db        440 GNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 11
US-10-849-615-69
; Sequence 69, Application US/10849615
; Publication No. US20050025764A1
; GENERAL INFORMATION:
;  APPLICANT: Allan, Barrett W.
;  APPLICANT:  Davies, Julian
;  APPLICANT:  Marquis, David M.
;  APPLICANT:  Ondek, Brian
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: CD20 BINDING MOLECULES
;  FILE REFERENCE: AME-09016
;  CURRENT APPLICATION NUMBER: US/10/849,615
;  CURRENT FILING DATE:  2004-05-20
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(451)
;   OTHER INFORMATION: AME 33 complete heavy chain
US-10-849-615-69

  Query Match             92.8%;  Score 2218;  DB 17;  Length 451;
  Best Local Similarity   93.3%;  Pred. No. 1e-140;
  Matches  421;  Conservative    7;  Mismatches   19;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||  |||| : |||||||||||| || |||   || |
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTGDTSY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY----FYFDLWGRGTLVTVS 116
              :   : |||||||||||||||||||||||||||||   :|    : ||:||:|| ||||
Db         61 NQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDWQFDVWGKGTTVTVS 120

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 240

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        421 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 12
US-10-216-484-157
; Sequence 157, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 157
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed
;   OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-216-484-157

  Query Match             90.5%;  Score 2164;  DB 14;  Length 470;
  Best Local Similarity   89.6%;  Pred. No. 4.6e-137;
  Matches  404;  Conservative   20;  Mismatches   23;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| ||| ||||| |||| ||:||| || | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYFYFDLWGRGTLVTVS 116
              :  |:|:|||: | | |||:: |||:: |||:|||       : :|||:|| |||||
Db         80 NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 13
US-10-384-933-157
; Sequence 157, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030170817A1ufusa
;  APPLICANT:  Haruyama, Hideyuki
```

; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 157
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed
; OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-384-933-157

Query Match 90.5%; Score 2164; DB 14; Length 470;
Best Local Similarity 89.6%; Pred. No. 4.6e-137;
Matches 404; Conservative 20; Mismatches 23; Indels 4; Gaps 1;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| ||| |||||: |||| ||:||| || | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYFYFDLWGRGTLVTVS 116
              :  |:|:|||: | | |||:: |||:: |||:|||       : :|||:||:|||||||
Db         80 NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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RESULT 14
US-10-216-484-147
; Sequence 147, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-147

Query Match 90.4%; Score 2160; DB 14; Length 470;
Best Local Similarity 89.1%; Pred. No. 8.5e-137;
Matches 402; Conservative 22; Mismatches 23; Indels 4; Gaps 1;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| ||| |||||: |||| ||:||| || | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYFYFDLWGRGTLVTVS 116
              :  |:|:|||: | | |||:: |||:: |||:|||       : :|||:||:|||||||
Db         80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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RESULT 15
US-10-384-933-147
; Sequence 147, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;   OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-147

  Query Match             90.4%;  Score 2160;  DB 14;  Length 470;
  Best Local Similarity   89.1%;  Pred. No. 8.5e-137;
  Matches  402;  Conservative   22;  Mismatches   23;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| ||| |||||: |||| ||:||| || | | || | |
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYFYFDLWGRGTLVTVS 116
              :  |:|: |:: | | ||||:: |||:: |||:|||       : :|||:||:|||||||
Db         80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


Search completed: September  8, 2005, 00:48:31
Job time : 112.328 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:01:25 ; Search time 30.6996 Seconds
(without alignments)
1086.923 Million cell updates/sec

Title: US-10-684-957-17
Perfect score: 2390
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2162	90.5	449	1	US-08-458-516-13	Sequence 13, Appl
2	2125.5	88.9	452	3	US-09-027-449-71	Sequence 71, Appl
3	2125.5	88.9	452	3	US-09-026-985-71	Sequence 71, Appl
4	2125.5	88.9	452	4	US-09-121-952A-71	Sequence 71, Appl
5	2125.5	88.9	452	4	US-09-234-340A-71	Sequence 71, Appl
6	2119	88.7	476	2	US-08-378-939-10	Sequence 10, Appl
7	2095.5	87.7	449	3	US-09-679-397-2	Sequence 2, Appli
8	2095.5	87.7	449	4	US-09-680-148-2	Sequence 2, Appli
9	2095.5	87.7	449	4	US-09-304-465A-2	Sequence 2, Appli
10	2092	87.5	468	3	US-09-485-737B-67	Sequence 67, Appl
11	2092	87.5	468	4	US-10-071-485-67	Sequence 67, Appl
12	2092	87.5	711	3	US-09-485-737B-90	Sequence 90, Appl
13	2092	87.5	711	4	US-10-071-485-90	Sequence 90, Appl
14	2089	87.4	466	4	US-09-698-705-11	Sequence 11, Appl
15	2083	87.2	451	2	US-08-887-352B-18	Sequence 18, Appl
16	2083	87.2	451	3	US-09-109-207C-18	Sequence 18, Appl
17	2083	87.2	451	3	US-09-282-505-2	Sequence 2, Appli
18	2083	87.2	451	3	US-09-054-255-2	Sequence 2, Appli
19	2083	87.2	451	3	US-09-296-005-18	Sequence 18, Appl
20	2083	87.2	451	4	US-09-282-846-2	Sequence 2, Appli
21	2083	87.2	451	4	US-09-680-145-2	Sequence 2, Appli
22	2083	87.2	451	4	US-09-920-171-18	Sequence 18, Appl
23	2083	87.2	451	4	US-09-716-028-18	Sequence 18, Appl
24	2083	87.2	451	4	US-09-483-588-2	Sequence 2, Appli
25	2083	87.2	451	4	US-10-113-996-18	Sequence 18, Appl
26	2082	87.1	451	2	US-08-887-352B-14	Sequence 14, Appl
27	2082	87.1	451	2	US-08-887-352B-16	Sequence 16, Appl
28	2082	87.1	451	3	US-08-466-151-65	Sequence 65, Appl
29	2082	87.1	451	3	US-09-109-207C-14	Sequence 14, Appl
30	2082	87.1	451	3	US-09-109-207C-16	Sequence 16, Appl
31	2082	87.1	451	3	US-09-296-005-14	Sequence 14, Appl
32	2082	87.1	451	3	US-09-296-005-16	Sequence 16, Appl
33	2082	87.1	451	4	US-09-920-171-14	Sequence 14, Appl
34	2082	87.1	451	4	US-09-920-171-16	Sequence 16, Appl
35	2082	87.1	451	4	US-09-716-028-14	Sequence 14, Appl
36	2082	87.1	451	4	US-09-716-028-16	Sequence 16, Appl
37	2082	87.1	451	4	US-10-113-996-14	Sequence 14, Appl
38	2082	87.1	451	4	US-10-113-996-16	Sequence 16, Appl
39	2081	87.1	472	4	US-09-301-593-43	Sequence 43, Appl
40	2077.5	86.9	467	3	US-09-049-672A-8	Sequence 8, Appli
41	2066	86.4	451	3	US-09-247-352-3	Sequence 3, Appli
42	2066	86.4	451	4	US-09-466-635-3	Sequence 3, Appli
43	2059	86.2	453	3	US-08-466-151-8	Sequence 8, Appli
44	2059	86.2	453	3	US-08-466-163B-8	Sequence 8, Appli
45	2059	86.2	453	4	US-09-802-096-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13

Query Match 90.5%; Score 2162; DB 1; Length 449;
Best Local Similarity 89.5%; Pred. No. 7.8e-167;
Matches 402; Conservative 23; Mismatches 22; Indels 2; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

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Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG--SGSYFYFDLWGRGTLVTVSSA 118

Db         61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSSA 120

Qy        119 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 178

Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        179 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 238

Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        239 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 298

Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        299 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 358

Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        359 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 418

Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        419 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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RESULT 2
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/027,449
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074,330
;      FILING DATE:  22-Jan-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/038,664
;      FILING DATE:  21-Feb-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R3-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-027-449-71

  Query Match             88.9%;  Score 2125.5;  DB 3;  Length 452;
  Best Local Similarity   87.6%;  Pred. No. 7.1e-164;
  Matches  396;  Conservative   26;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----FYFDLWGRGTLVTV 115

Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175

Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235

Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295

Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355

Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415

Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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RESULT 3
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/026,985
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
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;      REFERENCE/DOCKET NUMBER:  P1085R3-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-026-985-71

  Query Match             88.9%;  Score 2125.5;  DB 3;  Length 452;
  Best Local Similarity   87.6%;  Pred. No. 7.1e-164;
  Matches  396;  Conservative   26;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||  : :|| ||::||  |||:|:|::: |||| |||||| :| | | : :| |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----FYFDLWGRGTLVTV 115
              :  |:|: |:| | | :|||| :||:| |||:|||  | |      ::||:||:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              .:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 4
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952A
;      FILING DATE:  24-Jul-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-121-952A-71

  Query Match             88.9%;  Score 2125.5;  DB 4;  Length 452;
  Best Local Similarity   87.6%;  Pred. No. 7.1e-164;
  Matches  396;  Conservative   26;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||  : :|| ||::||  |||:|:|::: |||| |||||| :| | | : :| |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----FYFDLWGRGTLVTV 115
              :  |:|: |:| | | :|||| :||:| |||:|||  | |      ::||:||:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              .:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
```

```
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/234,340A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952
;      FILING DATE:  24-Jul-1998
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-234-340A-71

  Query Match             88.9%;  Score 2125.5;  DB 4;  Length 452;
  Best Local Similarity   87.6%;  Pred. No. 7.1e-164;
  Matches  396;  Conservative   26;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||  : :|| ||::||  |||:|:|::: |||| |||||| :| | | : :| |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-----FYFDLWGRGTLVTV 115
              :  |:|: |:| | | :||||| :||:| |||:|||  | |     ::||:||:||||||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        116 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        176 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 6
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-10

  Query Match             88.7%;  Score 2119;  DB 2;  Length 476;
  Best Local Similarity   87.5%;  Pred. No. 2.6e-163;
  Matches  400;  Conservative   21;  Mismatches   26;  Indels   10;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ::|:|||||||||||| |: :||| ||  |::| | |||| ||:||| || | |      |
Db         20 QMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYAISWVRQAPGQGLEWMGGIIPLFGTPTY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY----------FYFDLWGRG 110
              | :|||:|||:|||| |||::: :||:: |||:||| :  |           :|| ||:|
Db         80 SQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCATDRYRQANFDRARVGWFDPWGQG 139

Qy        111 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 199

Qy        171 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 259

Qy        231 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 319

Qy        291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 350
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 379

Qy        351 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 410
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 439

Qy        411 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
                |||||||||||||||||||||||||||||||||||||
Db        440 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476


RESULT 7
US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
;  APPLICANT: BASEY, CAROL D.
;  APPLICANT:  BLANK, GREG S.
;  TITLE OF INVENTION: PROTEIN PURIFICATION
;  FILE REFERENCE: P1241R1D2
;  CURRENT APPLICATION NUMBER: US/09/679,397
;  CURRENT FILING DATE:  2000-10-03
;  PRIOR APPLICATION NUMBER: US 60/084,459
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: US 09/304,465
;  PRIOR FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

  Query Match            87.7%;  Score 2095.5;  DB 3;  Length 449;
  Best Local Similarity  87.8%;  Pred. No. 1.9e-161;
  Matches  394;  Conservative   21;  Mismatches   31;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||:|    :| |||| |||||| :  ||| :  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              : | :|: ||||| | :||||| :||:| |||:|||   |   ::  | ||:||||||||
Db         61 ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 446
              ||||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 8
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
;  APPLICANT: BASEY, CAROL D.
;  APPLICANT:  BLANK, GREG S.
;  TITLE OF INVENTION: PROTEIN PURIFICATION
;  FILE REFERENCE: P1241R1D1
;  CURRENT APPLICATION NUMBER: US/09/680,148
;  CURRENT FILING DATE:  2000-10-03
;  PRIOR APPLICATION NUMBER: US 60/084,459
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: US 09/304,465
;  PRIOR FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2

  Query Match            87.7%;  Score 2095.5;  DB 4;  Length 449;
  Best Local Similarity  87.8%;  Pred. No. 1.9e-161;
  Matches  394;  Conservative   21;  Mismatches   31;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||:|    :| |||| |||||| :  ||| :  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              : | :|: ||||| | :||||| :||:| |||:|||   |   ::  | ||:||||||||
Db         61 ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 446
              ||||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 9
US-09-304-465A-2
; Sequence 2, Application US/09304465A
; Patent No. 6489447
; GENERAL INFORMATION:
;  APPLICANT: BASEY, CAROL D.
;  APPLICANT:  BLANK, GREG S.
;  TITLE OF INVENTION: PROTEIN PURIFICATION
;  FILE REFERENCE: P1241R1
;  CURRENT APPLICATION NUMBER: US/09/304,465A
;  CURRENT FILING DATE:  1999-05-03
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;  PRIOR APPLICATION NUMBER: US 60/084,459
;  PRIOR FILING DATE: 1998-05-06
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;    LENGTH: 449
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6489447
US-09-304-465A-2

  Query Match             87.7%;  Score 2095.5;  DB 4;  Length 449;
  Best Local Similarity   87.8%;  Pred. No. 1.9e-161;
  Matches  394;  Conservative   21;  Mismatches   31;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||:|    :| |||| ||||||  :  ||| :  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              : | :|: |||||  | :|||||  :||:|  |||:|||    |   ::   | ||:||||||||
Db         61 ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 446
              ||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 10
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/09/485,737B
;  CURRENT FILING DATE:  2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
;    LENGTH: 468
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

  Query Match             87.5%;  Score 2092;  DB 3;  Length 468;
  Best Local Similarity   87.5%;  Pred. No. 3.8e-161;
  Matches  391;  Conservative   20;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||:|:|||| |:|||| ||| || | : ||:| ||:||: || |     :: |
Db         21 QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGWINTYTGESTY 80

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                  |:|:   | | |:| |||| ||||| ||| |:|    ::  | ||:|| ||||||||
Db         81 VDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRGFYAMDYWGQGTTVTVSSAST 140

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 200

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        201 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 260

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 320

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              |||||||||||||||||||||||||||||| |||||||||||||||||||:|:||
Db        321 RVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTK 380

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 440

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        441 NVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 11
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
;  TITLE OF INVENTION:  SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/10/071,485
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: 09/485,737
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
;    LENGTH: 468
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

  Query Match             87.5%;  Score 2092;  DB 4;  Length 468;
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  Best Local Similarity   87.5%;  Pred. No. 3.8e-161;
  Matches  391;  Conservative   20;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||:|:|||| |:||||| ||| || | : ||:| ||:||: || |     :: |
Db         21 QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGWINTYTGESTY 80

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                 |:|:   | | |:| |||| ||||| ||| |:|    ::  | ||:|| ||||||||
Db         81 VDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRGFYAMDYWGQGTTVTVSSAST 140

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 200

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        201 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 260

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 320

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              |||||||||||||||||||||||||||| |||||||||||||||||||:|:||
Db        321 RVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTK 380

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 440

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||
Db        441 NVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 12
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/09/485,737B
;  CURRENT FILING DATE:  2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

  Query Match             87.5%;  Score 2092;  DB 3;  Length 711;
  Best Local Similarity   87.5%;  Pred. No. 6.8e-161;
  Matches  391;  Conservative   20;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||:|:|||| |:||||| ||| || | : ||:| ||:||: || |     :: |
Db         21 QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGWINTYTGESTY 80

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                 |:|:   | | |:| |||| ||||| ||| |:|    ::  | ||:|| ||||||||
Db         81 VDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRGFYAMDYWGQGTTVTVSSAST 140

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 200

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        201 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 260

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 320

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              |||||||||||||||||||||||||||| |||||||||||||||||||:|:||
Db        321 RVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTK 380

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 440

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||
Db        441 NVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 13
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
;  TITLE OF INVENTION:  SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/10/071,485
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: 09/485,737
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

  Query Match             87.5%;  Score 2092;  DB 4;  Length 711;
  Best Local Similarity   87.5%;  Pred. No. 6.8e-161;
  Matches  391;  Conservative   20;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||:|:|||| |:||||| ||| || | : ||:| ||:||: || |     :: |
Db         21 QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGWINTYTGESTY 80

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                 |:|:   | | |:| |||| ||||| ||| |:|    ::  | ||:|| ||||||||
Db         81 VDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRGFYAMDYWGQGTTVTVSSAST 140

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        141 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 200

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        201 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 260

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 320

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              |||||||||||||||||||||||||||| ||||||||||||||||||||:|:||
Db        321 RVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTK 380

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 440

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        441 NVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 14
US-09-698-705-11
; Sequence 11, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
;  APPLICANT:  Devaux, B.
;  APPLICANT:  Keller, G.
;  APPLICANT:  Koeppen, H.
;  APPLICANT:  Lasky, L.
;  TITLE OF INVENTION:  Anti-Tumor Antibody Compositions and Methods of Use
;  FILE REFERENCE:  P1777R1
;  CURRENT APPLICATION NUMBER: US/09/698,705
;  CURRENT FILING DATE:  2000-10-27
;  PRIOR APPLICATION NUMBER:  US 60/162,558
;  PRIOR FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  US 60/182,872
;  PRIOR FILING DATE:  2000-02-16
;  NUMBER OF SEQ ID NOS:  25
; SEQ ID NO 11
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-11

  Query Match             87.4%;  Score 2089;  DB 4;  Length 466;
  Best Local Similarity   86.6%;  Pred. No. 6.7e-161;
  Matches  387;  Conservative   23;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||: | |||: |||  :|:||| ||| ||:|| ||:| ||:||| :| | | ||:  |
Db         20 QVQVQQPGAELVKPGAPVKLSCKASGYTFTNYWLNWVKQRPGRGLEWIGRIDPSDSEIHY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
                 |: : |:: ||| ||||:| ||| : |:|:||| :    ||:|| |||||| |
Db         80 DQKFKDKATLTVDKSSSTAYIQLSSLTSEDSAVYYCALTGIYAMAYWGQGTSVTVSSAKT 139

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 199

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 259

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 319

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|:||
Db        320 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 379

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 439

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        440 NVFSCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 15
US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
;  APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of
;  TITLE OF INVENTION:  Improving Polypeptides
;  NUMBER OF SEQUENCES:  26
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  Genentech, Inc.
;    STREET:  1 DNA Way
;    CITY:  South San Francisco
;    STATE:  California
;    COUNTRY:  USA
;    ZIP:  94080
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  WinPatin (Genentech)
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/887,352B
;    FILING DATE:  03-Jul-1997
;    CLASSIFICATION:  530
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Svoboda, Craig G.
;    REGISTRATION NUMBER:  39,044
;    REFERENCE/DOCKET NUMBER:  P1123
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  650/225-1489
;    TELEFAX:  650/952-9881
; INFORMATION FOR SEQ ID NO:  18:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH:  451 amino acids
;    TYPE:  Amino Acid
;    TOPOLOGY:  Linear
US-08-887-352B-18

  Query Match             87.2%;  Score 2083;  DB 2;  Length 451;
  Best Local Similarity   87.2%;  Pred. No. 2e-160;
  Matches  395;  Conservative   25;  Mismatches   25;  Indels    8;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTS-YWIGWVRQMPGKGLE-LMGIIYPGDSDT 58
              |||||:||  : :|| ||::||  |||: || |   |:|| |||||| :  | | |  :|
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG--ET 58

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY----FDLWGRGTLVT 114
              :|:|| :|::||| | | :| ||| :||:| |||:||| ||::    | :||:|||||
Db         59 KYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVT 118

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
                |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
                |||||||||||||||||||||||||||||||||
Db        419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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Search completed: September 8, 2005, 00:15:42
Job time : 32.6996 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:15:52 ; Search time 108.629 Seconds
(without alignments)
2107.158 Million cell updates/sec

Title: US-10-684-957-17
Perfect score: 2390
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2126.5	89.0	469	2	Q7Z7P5	Q7z7p5 homo sapien
2	2091	87.5	480	2	Q6PJF1	Q6pjf1 homo sapien
3	2090.5	87.5	475	2	Q6N095	Q6n095 homo sapien
4	2085	87.2	470	2	Q6PJA4	Q6pja4 homo sapien
5	2080.5	87.1	475	2	Q6MZQ6	Q6mzq6 homo sapien
6	2079	87.0	478	2	Q6PI81	Q6pi81 homo sapien
7	2072	86.7	466	2	Q6N096	Q6n096 homo sapien
8	2063.5	86.3	544	2	Q6PJ95	Q6pj95 homo sapien
9	2060	86.2	466	2	Q6IN78	Q6in78 homo sapien
10	2060	86.2	472	2	Q6N089	Q6n089 homo sapien
11	2058.5	86.1	465	2	Q6GMX6	Q6gmx6 homo sapien
12	2058	86.1	480	2	Q6N094	Q6n094 homo sapien
13	2056.5	86.0	473	2	Q6P055	Q6p055 homo sapien
14	2043.5	85.5	473	2	Q6MZV7	Q6mzv7 homo sapien
15	2033.5	85.1	475	2	Q6GMW7	Q6gmw7 homo sapien
16	2029	84.9	482	2	Q7Z351	Q7z351 homo sapien
17	2026	84.8	470	2	Q7Z5W1	Q7z5w1 homo sapien
18	2018	84.4	476	2	Q6GMX1	Q6gmx1 homo sapien
19	2007.5	84.0	481	2	Q6N097	Q6n097 homo sapien
20	1985	83.1	518	2	Q6N030	Q6n030 homo sapien
21	1916.5	80.2	521	2	Q8N4Y9	Q8n4y9 homo sapien
22	1907.5	79.8	465	2	Q6P6C4	Q6p6c4 homo sapien
23	1882	78.7	464	2	Q6MZU6	Q6mzu6 homo sapien
24	1848	77.3	493	2	Q68CN4	Q68cn4 homo sapien
25	1824	76.3	473	2	Q8TC63	Q8tc63 homo sapien
26	1821	76.2	348	2	Q6PYX1	Q6pyx1 homo sapien
27	1815	75.9	417	2	Q6N093	Q6n093 homo sapien
28	1808.5	75.7	476	2	Q6MZX7	Q6mzx7 homo sapien
29	1767	73.9	330	1	GC1_HUMAN	P01857 homo sapien
30	1616.5	67.6	509	2	Q8NF17	Q8nf17 homo sapien
31	1604	67.1	326	1	GC2_HUMAN	P01859 homo sapien
32	1590.5	66.5	327	1	GC4_HUMAN	P01861 homo sapien
33	1540.5	64.5	487	2	Q65ZL2	Q65zl2 mus sp. fv/
34	1524.5	63.8	354	2	Q86TT2	Q86tt2 homo sapien
35	1512.5	63.3	463	2	Q99LC4	Q99lc4 mus musculu
36	1512	63.3	470	2	Q7TMK1	Q7tmk1 mus musculu
37	1499.5	62.7	473	2	Q9D8L4	Q9d8l4 mus musculu
38	1473.5	61.7	465	2	Q6PJB2	Q6pjb2 mus musculu
39	1466	61.3	464	2	Q6PF95	Q6pf95 mus musculu
40	1453	60.8	472	2	Q6PJA7	Q6pja7 mus musculu
41	1442	60.3	474	2	Q8R3H6	Q8r3h6 mus musculu
42	1411	59.0	458	2	Q65ZQ1	Q65zq1 homo sapien
43	1399.5	58.6	471	2	Q66K04	Q66k04 mus musculu
44	1392	58.2	464	2	Q6PIP8	Q6pip8 mus musculu
45	1369.5	57.3	473	2	Q91Z05	Q91z05 mus musculu

ALIGNMENTS

RESULT 1
Q7Z7P5
ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 89.0%; Score 2126.5; DB 2; Length 469;

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  Best Local Similarity   88.7%;  Pred. No. 2.5e-136;
  Matches  399;  Conservative   23;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :| |||||||||||| |:|:||| |||||:|| : |||| ||:||| || |   : ||:|
Db         20 QVHLVQSGAEVKKPGASVKLSCKTSGYNFSSYDLIWVRQAPGQGLEWMGWISAHNGDTKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS---GSYFYFDLWGRGTLVTVSS 117
              :  |||:||:: | | :|:|::: ||:: |||::|| :    |    || ||:|||||||
Db         80 ARKFQGRVTMTTDTSATTSYMEFRSLRSDDTALFYCATKSRGQVGDFDSWGQGTLVTVSS 139

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 199

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 259

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 379

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 439

Qy'       418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||
Db        440 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469


RESULT 2
Q6PJF1
ID   Q6PJF1      PRELIMINARY;      PRT;   480 AA.
AC   Q6PJF1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016381; AAH16381.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   480 AA;  52586 MW;  64DC641AE47CD6C8 CRC64;

  Query Match             87.5%;  Score 2091;  DB 2;  Length 480;
  Best Local Similarity   86.1%;  Pred. No. 6.5e-134;
  Matches  397;  Conservative   21;  Mismatches   29;  Indels   14;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||| |:|:||| || :  |: | |||| ||:||  || | |   |:|
Db         20 QVQLVQSGAEVKKPGSSVKVSCKASGGSPGSFVISWVRQAPGQGLAWMGGIIPAFDITKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG---------SG-----SYFYFDL 106
              : :|| :|||||:|  |||::  ||:: ||| |||           ||       |:  |:
Db         80 AQNFQDRVTISADESTDTAYMELRSLRSEDTATYYCARDLALYELWSGFHTDEKYYGLDV 139

Qy        107 WGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 166
              ||:|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 WGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 199

Qy        167 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 226
              |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db        200 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTC 259

Qy        227 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319

Qy        287 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 379

Qy        347 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 406
              |||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||
Db        380 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 439

Qy        407 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||||||||||
Db        440 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 480


RESULT 3
Q6N095
ID   Q6N095      PRELIMINARY;      PRT;   475 AA.
AC   Q6N095;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686K03196.
GN   Name=DKFZp686K03196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
```

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RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640621; CAE45775.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52360 MW;  7BA14104CD2DB8F0 CRC64;

  Query Match           87.5%;  Score 2090.5;  DB 2;  Length 475;
  Best Local Similarity   86.2%;  Pred. No. 7e-134;
  Matches  393;  Conservative   25;  Mismatches   29;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||:|:|| |: |||: |||:|::| | |||| ||: || |||: |       |
Db         20 QVQLVQSGAELKRPGASVTISCRASGYSFSTYHIHWVRQAPGQRLEWMGIMNPRSDSKTY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYF----YFDLWGRGT 111
              : :|||::|:: | | || ::: :|||: |||:|||     |   :|     ||:||:||
Db         80 AQTFQGRMTMTRDTSTSTVFMELNSLKSGDTAVYYCTRDRSGRALWFGELDAFDIWGQGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWVSNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 4
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match           87.2%;  Score 2085;  DB 2;  Length 470;
  Best Local Similarity   87.6%;  Pred. No. 1.6e-133;
  Matches  395;  Conservative   20;  Mismatches   32;  Indels    4;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||: |:|||: |||| |||||| :  |     |:  |
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFY---FDLWGRGTLVTVS 116
                | :|: ||| | : :: ||| :||:| |||:|||   || :|   || ||:|||||||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139

Qy        117 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        177 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 259

Qy        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        297 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379

Qy        357 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
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Qy        417 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 5
Q6MZQ6
ID   Q6MZQ6      PRELIMINARY;      PRT;   475 AA.
AC   Q6MZQ6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686G11190.
GN   Name=DKFZp686G11190;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640947; CAE45972.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52043 MW;  B7EAE255A26F4B8E CRC64;

  Query Match             87.1%;  Score 2080.5;  DB 2;  Length 475;
  Best Local Similarity   86.0%;  Pred. No. 3.3e-133;
  Matches  392;  Conservative   22;  Mismatches   33;  Indels    9;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||::||  : :|| ||::||  ||: | :| : |||| |||||  :  |     :| |
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMNWVRQAPGKGLEWVSGISSSGVNTYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG---------SGSYFYFDLWGRGT 111
              : | :|: ||| | | :| |||  ||:| |||:|||         | :|:|||:|||||
Db         80 ADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              ||:||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 6
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match             87.0%;  Score 2079;  DB 2;  Length 478;
  Best Local Similarity   85.0%;  Pred. No. 4.3e-133;
  Matches  390;  Conservative   23;  Mismatches   34;  Indels   12;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||: |:|||: |||| ||||||  :  |     |:  |
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC------------GSGSYFYFDLWG 108
                | :|: ||| | : :: ||| :||:| |||:|||                ||| |:||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139
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Qy        109 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 168
              :|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy        169 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 228
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP 259

Qy        229 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy        289 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy        349 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 408
              |||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439

Qy        409 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||||||||
Db        440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 7
Q6N096
ID   Q6N096      PRELIMINARY;      PRT;   466 AA.
AC   Q6N096;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I15196.
GN   Name=DKFZp686I15196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640620; CAE45774.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   466 AA;  50926 MW;  01E91B748D6D57C4 CRC64;

  Query Match           86.7%;  Score 2072;  DB 2;  Length 466;
  Best Local Similarity  87.0%;  Pred. No. 1.2e-132;
  Matches  389;  Conservative   21;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| |||:||  ||:   :||:  ||| |||||  : ::    |:| |
Db         20 EVQLVESGGGLVQPGGSLKLSCAASGFTVNNYWMHRVRQAPGKGLVWVSLMRDDASETAY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              :   ||: ||| | : :| :|| |||:| |||:|||  | :  || ||:||||||||||
Db         80 AEFVQGRFTISRDNAKNTLFLQLSSLRAEDTAVYYCARGGFGNFDQWGQGTLVTVSSAST 139

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 199

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 259

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 319

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        320 RVVSVLTVLHQDWLNGKEYKCRVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 379

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 439

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||| |||||||||||||||
Db        440 NVFSCSVMHEGLHNHYTQKSLSLSPGK 466
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RESULT 8
Q6PJ95
ID   Q6PJ95      PRELIMINARY;      PRT;   544 AA.
AC   Q6PJ95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019046; AAH19046.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   544 AA;  60102 MW;  1895814B2297C668 CRC64;

  Query Match           86.3%;  Score 2063.5;  DB 2;  Length 544;
  Best Local Similarity   86.1%;  Pred. No. 5.6e-132;
  Matches  391;  Conservative   20;  Mismatches   34;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              : |||:||  | :|| ||::||  ||: |::| : |||| |||||| : :    :||  |
Db         20 QAQLVESGGGVVQPGSSLRLSCAASGFRFSNYGMHWVRQAPGKGLEWVAVFSYDESDKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-------SGSYFY--FDLWGRGT 111
              : | :|: ||| | | :|  || :||:  |||:|||       | |:|   || |||||
Db         80 AASVKGRFTISRDNSKNTLSLQMNSLRVEDTAVYYCAKDQKPWYSNSWFLTNFDSWGRGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 445
              ||||||||||||||||||||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 473


RESULT 9
Q6IN78
ID   Q6IN78      PRELIMINARY;      PRT;   466 AA.
AC   Q6IN78;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072419; AAH72419.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   466 AA;  50853 MW;  53EB0BCEDE81076E CRC64;

  Query Match           86.2%;  Score 2060;  DB 2;  Length 466;
  Best Local Similarity   87.3%;  Pred. No. 8.1e-132;
  Matches  391;  Conservative   21;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| || :||  ||   :| :: |||| |||||| : ::| | : | |
Db         20 EVQLVESGGGLIQPGGSLTLSCAASGLTVSSNYMHWVRQAPGKGLEWVSVLYIGGA-TYY 78

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY-FDLWGRGTLVTVSSAS 119
              : | :|: ||| | | :| ||| :||:| |||:|||  |:|      ||:||||||||||
Db         79 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGNYVVPAAPWGQGTLVTVSSAS 138

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 198

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 239
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        199 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPS 258

Qy        240 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 318

Qy        300 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 378

Qy        360 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 438

Qy        420 GNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||
Db        439 GNVFSCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 10
Q6N089
ID   Q6N089      PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
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DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             86.2%;  Score 2060;  DB 2;  Length 472;
  Best Local Similarity   85.7%;  Pred. No. 8.2e-132;
  Matches  388;  Conservative   24;  Mismatches   35;  Indels    6;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  ||: |  | : |||| |||||| :  |          |
Db`        20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYFYF--DLWGRGTLVT 114
              : | :|: ||| |   :: ||| :||:| |||:|||    |: :::|:  |:||:|| ||
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAKEIGAHNFYYYGMDVWGQGTTVT 139

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 199

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        200 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEL 259

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 319

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 379

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 439

Qy        415 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        440 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 11
Q6GMX6
ID   Q6GMX6      PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;

  Query Match             86.1%;  Score 2058.5;  DB 2;  Length 465;
  Best Local Similarity   86.8%;  Pred. No. 1e-131;
  Matches  388;  Conservative   22;  Mismatches   36;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||| :||  : || |:| ::|  || : : |:  |:||  ||||| :| ||   | | |
Db         20 QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPAGKGLEWIGRIYTSGS-TNY 78

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              :|| : :||:| | | :   |: ||: |:|||:|||  | : ||| ||:||||||||||
Db         79 NPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGRFTYFDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
                 ||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 12
Q6N094
ID   Q6N094      PRELIMINARY;      PRT;   480 AA.
AC   Q6N094;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686O01196.
GN   Name=DKFZp686O01196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640622; CAE45776.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   480 AA;  52612 MW;  225247F3D35AEC18 CRC64;

  Query Match             86.1%;  Score 2058;  DB 2;  Length 480;
  Best Local Similarity   83.9%;  Pred. No. 1.1e-131;
  Matches  387;  Conservative   23;  Mismatches   37;  Indels   14;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              | :||:||  : ||||||::||  ||: | |: : |||| |||||| :  |    ::  |
Db         20 EEELVESGGGLVKPGESLRLSCAASGFTFRSFNMNWVRQAPGKGLEWIAFINSRGNEKYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYF--------------YFDL 106
                | :|: ||| | : :: :|| |||:  |||:|||  | :               :||
Db         80 GESVKGRFTISRDNADNSLFLQMSSLRVDDTAIYYCARGKWVPAGPTSTSGPVRHNWFDP 139

Qy        107 WGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 166
              ||:||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 WGQGTLVTISSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 199

Qy        167 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 259

Qy        227 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319

Qy        287 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 379

Qy        347 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 439

Qy        407 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||| ||||||||||||||
Db        440 YSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 480


RESULT 13
Q6P055
ID   Q6P055      PRELIMINARY;      PRT;   473 AA.
AC   Q6P055;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC065820; AAH65820.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51344 MW;  9816D56A77129B57 CRC64;
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  Query Match           86.0%;  Score 2056.5;  DB 2;  Length 473;
  Best Local Similarity  85.7%;  Pred. No. 1.4e-131;
  Matches  389;  Conservative   17;  Mismatches   41;  Indels    7;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGD--SDT 58
              |  ||:||  : :|| || :|| |||: |:  |: |||| |||||| :  |   |    |
Db         20 EAHLVESGGGLVRPGGSLTLSCTGSGFTFSGAWLSWVRQAPGKGLEWVARIQTEDDGGTT 79

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS-----YFYFDLWGRGTLV 113
              |  : :|: |:| | | :| ||| | |:  ||| |:| :||         || ||:||||
Db         80 HYGIAVKGRFTVSRDDSRNTLYLQMSDLRTEDTAFYFCATGSMNTVGLTGFDSWGQGTLV 139

Qy        114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 199

Qy        174 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 259

Qy        234 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        294 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        354 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        414 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||| ||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 473
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RESULT 14
Q6MZV7
ID   Q6MZV7      PRELIMINARY;      PRT;   473 AA.
AC   Q6MZV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   Name=DKFZp686C11235;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RG   The German Human cDNA Consortium;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;
```

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  Query Match           85.5%;  Score 2043.5;  DB 2;  Length 473;
  Best Local Similarity  84.6%;  Pred. No. 1.1e-130;
  Matches  384;  Conservative   28;  Mismatches   35;  Indels    7;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |:|||:||  : :|| ||::||  ||: |:|: : |||| |||||| :  |   :  |
Db         20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-----SGSYF--YFDLWGRGTLV 113
              : | ||: ||| | : :: ||| :||:| |||:|||      :  ::  :|| ||:| ||
Db         80 ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV 139

Qy        114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSWNSGALTSGVHTFPAV 199

Qy        174 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 233
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 259

Qy        234 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        294 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        354 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 413
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        414 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473
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RESULT 15
Q6GMW7
ID   Q6GMW7      PRELIMINARY;      PRT;   475 AA.
AC   Q6GMW7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073782; AAH73782.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  51987 MW;  2A1FE55D736860F8 CRC64;

  Query Match            85.1%;  Score 2033.5;  DB 2;  Length 475;
  Best Local Similarity   84.4%;  Pred. No. 5.2e-130;
  Matches  385;  Conservative   21;  Mismatches   41;  Indels    9;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:||  : :|| ||::||  | :  : : : |||| |||||| :  |   :: | |
Db         20 EVQLVESGGGLVQPGGSLRLSCVASAFTLSRHAMHWVRQAPGKGLEYVSGISNSENSTYY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS---------YFYFDLWGRGT 111
              : | :|: ||| |   :| |||  ||:| | |:|||             |:  |:||:||
Db         80 ADSVKGRFTISRDNYKNTLYLQLGSLRAEDKAVYYCARARCRGDTCLNFYYGLDVWGQGT 139

Qy        112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 171
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        172 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        232 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        292 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        352 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        412 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


Search completed: September  8, 2005, 00:54:01
Job time : 111.629 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:34:28 ; Search time 24.2898 Seconds
(without alignments)
1770.656 Million cell updates/sec

Title: US-10-684-957-17
Perfect score: 2390
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1767	73.9	330	1	GHHU	Ig gamma-1 chain C
2	1630.5	68.2	377	2	A23511	Ig gamma-3 chain C
3	1628.5	68.1	377	2	A60764	Ig gamma-3 chain C
4	1604	67.1	326	1	G2HU	Ig gamma-2 chain C
5	1590.5	66.5	327	1	G4HU	Ig gamma-4 chain C
6	1474	61.7	446	2	S40295	Ig gamma-2a chain
7	1464.5	61.3	469	2	S37483	Ig gamma-2a chain
8	1435	60.0	374	2	S69339	Ig heavy chain V r
9	1419	59.4	470	2	S22080	Ig heavy chain pre
10	1411.5	59.1	444	2	PC4436	monoclonal antibod
11	1401	58.6	472	2	S31459	Ig gamma-1 chain -
12	1387.5	58.1	475	2	S01321	Ig gamma-2b chain
13	1386	58.0	474	1	G2MS11	Ig gamma-2b chain
14	1263	52.8	328	2	I47159	Ig gamma 2a chain
15	1260	52.7	255	4	S31866	Ig gamma-1 chain C
16	1257	52.6	328	2	I47160	Ig gamma 2b chain
17	1254	52.5	234	2	PT0207	Ig gamma chain C r
18	1231	51.5	328	2	I47158	Ig gamma 1 chain c
19	1230.5	51.5	323	1	GHRB	Ig gamma chain C r
20	1227	51.3	328	2	I47161	Ig gamma 3 chain c
21	1216.5	50.9	329	1	G2GP	Ig gamma-2 chain C
22	1161.5	48.6	308	2	C30554	Ig heavy chain C r
23	1152	48.2	326	2	PS0017	Ig gamma-1 chain C
24	1151	48.2	289	1	G3HUWI	Ig gamma-3 heavy c
25	1146.5	48.0	333	2	PS0018	Ig gamma-2b chain
26	1142	47.8	324	1	G1MS	Ig gamma-1 chain C
27	1141	47.7	329	1	G3MSC	Ig gamma-3 chain C
28	1137	47.6	393	1	G1MSM	Ig gamma-1 chain C
29	1130	47.3	398	1	G3MSM	Ig gamma-3 chain C
30	1126	47.1	330	1	G2MSA	Ig gamma-2a chain
31	1123.5	47.0	335	1	G2MSAB	Ig gamma-2a chain
32	1121	46.9	399	1	G2MSAM	Ig gamma-2a chain
33	1118.5	46.8	329	2	S00847	Ig gamma-2c chain
34	1112	46.5	322	2	PS0019	Ig gamma-2a chain
35	1092.5	45.7	327	2	S06611	Ig gamma-2 chain C
36	1082	45.3	405	1	G2MSBM	Ig gamma-2b chain
37	1066	44.6	277	2	I47162	Ig gamma 4 chain c
38	970	40.6	548	2	S38864	Ig epsilon chain C
39	937.5	39.2	549	2	S04845	Ig heavy chain pre
40	808.5	33.8	241	2	S69131	Ig heavy chain (DO
41	799	33.4	627	2	S14683	Ig mu chain precur
42	787	32.9	246	2	S38950	Ig gamma chain - m
43	772	32.3	220	2	A49444	Ig gamma-1 heavy c
44	754.5	31.6	572	2	B46529	Ig Y heavy chain (
45	730.5	30.6	249	2	S69340	Ig heavy chain VHI

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

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  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
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Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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```
RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             68.2%;  Score 1630.5;  DB 2;  Length 377;
  Best Local Similarity   82.0%;  Pred. No. 1.7e-88;
  Matches  309;  Conservative   10;  Mismatches   11;  Indels   47;  Gaps    1;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
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Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 215
              |||||||||||||||||||| ||||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy        216 ------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 250
                                      ||||||    || ||||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        251 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 310
              |||||||||||||||||||||:| ||||||||||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        311 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 370
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Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        371 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 430
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Db        301 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy        431 ALHNHYTQKSLSLSPGK 447
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Db        361 ALHNRFTQKSLSLSPGK 377


RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
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F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match            68.1%;  Score 1628.5;  DB 2;  Length 377;
  Best Local Similarity  82.0%;  Pred. No. 2.2e-88;
  Matches  309;  Conservative   10;  Mismatches   11;  Indels   47;  Gaps    1;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
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Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 215
              |||||||||||||||||||| |||||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy        216 ------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 250
                                       ||||||    || ||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        251 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 310
              |||||||||||||||||||||:| ||||||||||||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        311 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 370
              |||||||||||||||||||||||||| ||||||||||||||:|:||||||||||||
Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        371 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 430
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Db        301 GFYPSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

Qy        431 ALHNHYTQKSLSLSPGK 447
              |||| :||||||||||
Db        361 ALHNRFTQKSLSLSPGK 377


RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            67.1%;  Score 1604;  DB 1;  Length 326;
  Best Local Similarity  91.2%;  Pred. No. 5.1e-87;
  Matches  301;  Conservative   12;  Mismatches   13;  Indels    4;  Gaps    2;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              ||||||||||||| |:||| ||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              |||||||||||||: ||||| |||:|||||||||| || | | :  ||||||  : |
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||:|
Db        117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||:|||||||:|||||||||||||| |||||||||| |||||||||||||||||||:|
Db        177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              :||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||
Db        297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
```

```
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             66.5%;  Score 1590.5;  DB 1;  Length 327;
  Best Local Similarity   90.9%;  Pred. No. 3.2e-86;
  Matches  300;  Conservative   12;  Mismatches   15;  Indels    3;  Gaps    1;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              |||||||||||||| |:||| ||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
              |||||||||||||||||:|| |||:||||||||:|| |       || ||||| |||
Db         61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
              |||||||||||||||||||||||||||||| |||||:|||||||||||||||||||||:|
Db        118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              |||||||||||||||||||||||||||||| ||: ||||||||||||||||||||::|
Db        178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
              :||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db        238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |:|||||||||||||||||||||||| ||
Db        298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 6
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
A;Cross-references: UNIPROT:Q99L25
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             61.7%;  Score 1474;  DB 2;  Length 446;
  Best Local Similarity   61.2%;  Pred. No. 3e-79;
  Matches  274;  Conservative   66;  Mismatches  104;  Indels    4;  Gaps    3;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ::|| ||| |: :|| |:||||| ||| || |:| ||:| ||:||| :| ||||  :|:|
Db          1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              :  |:|: |:: | | ||||:| ||| : |:|:|:|  |  |  | ||:|| ||||||
Db         61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSSAKT 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              |||:|||| |:| :  |||||| |||||||::||||:|:|||||||||||  ||
Db        121 TAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-LY 179

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELLGGP 238
              :||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  |||| |||||
Db        180 TLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGP 238

Qy        239 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 298
              |||:|||| || |||| :| |||||||| :||:|: :|:|: |||  |:|:   | |||
Db        239 SVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNS 298

Qy        299 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 358
              | |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||  :|:
Db        299 TLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEM 358

Qy        359 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 418
              || ||:|||:|  | | || ||| :||: | ||| | ||||||||:|:|||| |:|  |
Db        359 TKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWV 418

Qy        419 QGNVFSCSVMHEALHNHYTQKSLSLSPG 446
              : | :||||:|| ||||:| || | :||
Db        419 ERNSYSCSVVHEGLHNHHTTKSFSRTPG 446


RESULT 7
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>
```

```
  Query Match           61.3%;  Score 1464.5;  DB 2;  Length 469;
  Best Local Similarity  60.4%;  Pred. No. 1.1e-78;
  Matches  273;  Conservative   68;  Mismatches  104;  Indels    7;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ::|| ||| |: ||| |:|||| ||| || |:| ||:| ||:||: :| |||   :|:|
Db         20 QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKPGQGLKWIGWIYPASGNTKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG---SGSYFYFDLWGRGTLVTVSS 117
              : :|:|: |:: | | ||||:| ||| : |||:|:|     :    | ||:|| :||||
Db         80 NENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCARAMGATATLLDYWGQGTTLTVSS 139

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              | |  |||:|||| |:| :  |||||| |||||||::||||:|:|||||||||||||
Db        140 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 199

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 235
              ||:||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  |||| ||
Db        200 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 257

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295
              ||||||:|||| || |||| :| ||||||||| :||:|: :|:|: |||| |:|:   |
Db        258 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 317

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355
              |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||
Db        318 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 377

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415
              :|:|| ||:|||:|  | | || ||| :||: | ||| | |||||||:|:|||| |:|
Db        378 EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 437

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              | : | :||||:|| ||||:| || | :|||
Db        438 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 469


RESULT 8
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match           60.0%;  Score 1435;  DB 2;  Length 374;
  Best Local Similarity  61.5%;  Pred. No. 4.7e-77;
  Matches  279;  Conservative   30;  Mismatches   39;  Indels  106;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNF--TSYWIGWVRQMPGKGLELMGIIYPGDSDT 58
              :: | :||  : || ::| ::|  ||::   :   :||:|| ||: || : :|:  | |
Db         20 QITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALEWLALIF-WDDDK 78

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC-----GSGSYFYFDLWGRGTLV 113
              ||||| : ::||: | | :   |  :::  :||| |||     | |  : |  ||:||||
Db         79 RYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLV 138

Qy        114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
              ||||
Db        139 TVSS---------------------------------------------------------- 142

Qy        174 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 233
                                                   ||||||||||||||||||
Db        143 ----------------------------------------EPKSCDKTHTCPPCPAPE 160

Qy        234 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 220

Qy        294 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 280

Qy        354 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 413
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 340

Qy        414 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||
Db        341 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374


RESULT 9
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           59.4%;  Score 1419;  DB 2;  Length 470;
  Best Local Similarity  60.4%;  Pred. No. 5.3e-76;
  Matches  275;  Conservative   59;  Mismatches  109;  Indels   12;  Gaps    6;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||| :||  : || ::| ::|  ||:: :|| : |||| ||| || :| |  | : | |
Db         20 QVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWVGGITSGGT-TYY 78

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY------FYFDLWGRGTLVT 114
              :|: : :::|: : | |   |  ||:   ||| |||   :|       | ||:| |||
Db         79 NPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAWGQGLLVT 138

Qy        115 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 174
              ||||||  | |:||:      |  |  |||||  | |||||:|||||| ||||||||||
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Db        139 VSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYMPEPVTVTWNSGALKSGVHTFPAVL 198

Qy        175 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 234

Db        199 QSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPPEL 255

Qy        235 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 294

Db        256 PGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPREE 315

Qy        295 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 354

Db        316 QFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPP 375

Qy        355 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 412

Db        376 QEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQLDADSSYFLYSKLRV 435

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        436 DRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK 470


RESULT 10
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

  Query Match           59.1%;  Score 1411.5;  DB 2;  Length 444;
  Best Local Similarity   58.0%;  Pred. No. 1.4e-75;
  Matches  262;  Conservative   77;  Mismatches  100;  Indels   13;  Gaps    6;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSD--T 58

Db          1 EVQXVETGGGLVRPGNSLKLSCLTSGFTFSNYRMHWLRQPPGKRLEWIAVITVKSDNYGA 60

Qy         59 RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY-FDLWGRGTLVTVSS 117

Db         61 KYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTPWVYAMDCWGQGTSVIVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177

Db        121 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 235

Db        181 -LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 234

Qy        236 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 295

Db        235 --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 292

Qy        296 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 355

Db        293 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 352

Qy        356 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 415

Db        353 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKS 412

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        413 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444


RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

  Query Match           58.6%;  Score 1401;  DB 2;  Length 472;
  Best Local Similarity   58.3%;  Pred. No. 6e-75;
  Matches  268;  Conservative   65;  Mismatches  109;  Indels   18;  Gaps    5;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPG---DSD 57

Db         18 QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWLG----GSGYDED 73

Qy         58 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG--------SGSYFYFDLWGR 109

Db         74 IDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWGP 133

Qy        110 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 169

Db        134 GLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVHT 193

Qy        170 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC 229

Db        194 FPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-RC 252

Qy        230 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 289

Db        253 PPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTART 312

Qy        290 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 349

Db        313 KPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQVY 372

Qy        350 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLY 407

Db        373 VLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFLY 432

Qy        408 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        433 SRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472


RESULT 12
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
```

```
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

  Query Match             58.1%;  Score 1387.5;  DB 2;  Length 475;
  Best Local Similarity   57.8%;  Pred. No. 3.7e-74;
  Matches  264;  Conservative   70;  Mismatches  112;  Indels   11;  Gaps    4;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||| |||||: :|| |:|:||| |||  ||| | ||:|  |:||| :| ||||  :: :
Db         20 QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG---SYFYFDLWGRGTLVTVSS 117
              :  |:|: |:: ||| |||||  ||| : |:|:|:|           |  ||:||||| |:
Db         80 NEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPFGYWGQGTLVTASA 139

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
              | |  |||:|||    |:| :  |||||| |||| |||:||||:|:| |||||||:|| |
Db        140 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S 198

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------CP 230
              |||::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||      ||
Db        199 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCKECHKCP 258

Qy        231 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290
              || | ||||||:|||  || |||| ||:||||||||| :||:|: :|:|: |||  |:|:
Db        259 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQ 318

Qy        291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 350
              | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | ||||
Db        319 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKIKGIVRAPQVYI 378

Qy        351 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 410
              | |  ::|::  |||||  || | ||:||| |||  | ||| | ||||||||:|:||||
Db        379 LSPPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 438

Qy        411 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              :  |:|:: : |||:| || | |:| :|::| ||||
Db        439 NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 475


RESULT 13
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             58.0%;  Score 1386;  DB 1;  Length 474;
  Best Local Similarity   57.1%;  Pred. No. 4.6e-74;
  Matches  260;  Conservative   73;  Mismatches  114;  Indels    8;  Gaps    3;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||| ||| |:  || |:|:||| ||| | :| : ||:| ||:||| :| | |    |::
Db         20 EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG-SYFYFDLWGRGTLVTVSSAS 119
              :  |:|: |:::||| :|||:: ||| : |:|:|||     | :|  ||:||||||:|
Db         80 NEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARDYDYDWFAYWGQGTLVTVSAAK 139

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
              |  |||:|||    |:| :  ||||| |||| |||:||||:|:| |||    |  |||
Db        140 TTPPSVYPLAPGCGDTTGSSVTSGCLVKGYFPESVTVTWNSGSLSSSVHTLSQALLQSGL 199

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------CPAP 232
              |::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||      ||||
Db        200 YTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAP 259

Qy        233 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 292
              | ||||||:|||  || |||| ||:||||||||| :||:|: :|:|: |||| |:|:
Db        260 NLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH 319

Qy        293 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 352
              | |||| |||| | : ||||::|||:||||:|| ||:|||:|||| ||  | |||| ||
```

```
Db        320 REDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILP 379

Qy        353 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 412

Db        380 PPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM 439

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        440 KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474


RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             52.8%;  Score 1263;  DB 2;  Length 328;
  Best Local Similarity   69.6%;  Pred. No. 4.8e-67;
  Matches  231;  Conservative   43;  Mismatches   52;  Indels    6;  Gaps    2;

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177

Db          1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPPEPVTVTWNSGALSSGVHTFPSVLQPS 60

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237

Db         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297

Db        117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357

Db        177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 415

Db        237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

Qy        416 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

  Query Match             52.7%;  Score 1260;  DB 4;  Length 255;
  Best Local Similarity   97.5%;  Pred. No. 5.4e-67;
  Matches  233;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        209 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 268

Db         17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

Qy        269 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 328

Db         77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136

Qy        329 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 388

Db        137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy        389 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

Db        197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255


Search completed: September  8, 2005, 00:55:17
Job time : 25.2898 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2005, 00:11:22 ; Search time 120.437 Seconds
(without alignments)
1435.455 Million cell updates/sec

Title: US-10-684-957-17
Perfect score: 2390
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....MHEALHNHYTQKSLSLSPGK 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2390	100.0	447	8	ADS87924	Ads87924 Anti-IFN-
2	2390	100.0	447	8	ADS94921	Ads94921 Anti-IFN-
3	2379	99.5	447	8	ADS87928	Ads87928 Anti-IFN-
4	2379	99.5	447	8	ADS94925	Ads94925 Anti-IFN-
5	2374	99.3	447	8	ADS87926	Ads87926 Anti-IFN-
6	2374	99.3	447	8	ADS94923	Ads94923 Anti-IFN-
7	2360	98.7	447	8	ADS87939	Ads87939 Anti-IFN-
8	2360	98.7	447	8	ADS94936	Ads94936 Anti-IFN-
9	2286.5	95.7	468	8	ADR46819	Adr46819 Human ant
10	2286.5	95.7	613	8	ADR46827	Adr46827 Human bet
11	2273	95.1	474	4	AAU14177	Aau14177 Human nov
12	2258.5	94.5	467	8	ADM41567	Adm41567 Anti-inte
13	2181.5	91.3	450	8	ADS18704	Ads18704 Protein s
14	2176.5	91.1	450	8	ADS18702	Ads18702 Protein s
15	2176.5	91.1	450	8	ADS18708	Ads18708 Protein s
16	2175.5	91.0	450	8	ADS18710	Ads18710 Protein s
17	2167.5	90.7	450	8	ADS18706	Ads18706 Protein s
18	2164	90.5	470	3	AAW90936	Aaw90936 Humanised
19	2164	90.5	470	5	ABB74945	Abb74945 Humanised
20	2162	90.5	449	2	AAR43339	Aar43339 Completel
21	2162	90.5	449	2	AAW49816	Aaw49816 Amino aci
22	2160	90.4	470	3	AAW90935	Aaw90935 Humanised
23	2160	90.4	470	5	ABB74904	Abb74904 Mouse hum
24	2159.5	90.4	731	4	AAM52156	Aam52156 Humanised
25	2159.5	90.4	741	4	AAM52159	Aam52159 Humanised
26	2159	90.3	470	3	AAW90934	Aaw90934 Humanised
27	2159	90.3	470	5	ABB74903	Abb74903 Mouse hum
28	2157	90.3	448	6	ABR55871	Abr55871 Human imm
29	2157	90.3	448	8	ADN49728	Adn49728 Human imm
30	2157	90.3	451	8	ADF11670	Adf11670 anti-CD11
31	2157	90.3	470	3	AAW90933	Aaw90933 Humanised
32	2157	90.3	470	5	ABB74902	Abb74902 Humanised
33	2156	90.2	470	2	AAW83037	Aaw83037 Anti-Fas
34	2156	90.2	470	3	AAB14779	Aab14779 Humanised
35	2156	90.2	470	3	AAW90929	Aaw90929 Humanised
36	2156	90.2	470	5	ABB74944	Abb74944 Humanised
37	2156	90.2	470	5	ABB74898	Abb74898 Humanised
38	2154.5	90.1	471	8	ADP79584	Adp79584 2H7.v16 H
39	2154.5	90.1	729	4	AAM52158	Aam52158 Humanised
40	2154.5	90.1	739	4	AAM52161	Aam52161 Humanised
41	2153.5	90.1	445	8	ADJ11308	Adj11308 BHA10 VH#
42	2153.5	90.1	464	8	ADJ11354	Adj11354 BHA10 VL#
43	2150.5	90.0	450	6	ABG74713	Abg74713 Murine hu
44	2149.5	89.9	450	7	ABR83153	Abr83153 Hu007 ant
45	2149	89.9	447	8	ADQ31276	Adq31276 Humanised

ALIGNMENTS

RESULT 1
ADS87924
ID ADS87924 standard; protein; 447 AA.
XX
AC ADS87924;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 17; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36

```
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             100.0%;  Score 2390;  DB 8;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-140;
  Matches  447;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 2
ADS94921
ID   ADS94921 standard; protein; 447 AA.
XX
AC   ADS94921;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 14; SEQ ID NO 17; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             100.0%;  Score 2390;  DB 8;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-140;
  Matches  447;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
```

```
Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 3
ADS87928
ID ADS87928 standard; protein; 447 AA.
XX
AC ADS87928;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 21; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

```
  Query Match             99.5%;  Score 2379;  DB 8;  Length 447;
  Best Local Similarity   99.6%;  Pred. No. 4.5e-139;
  Matches  445;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

RESULT 4
ADS94925
ID ADS94925 standard; protein; 447 AA.
XX
AC ADS94925;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.

```
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 14; SEQ ID NO 21; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             99.5%;  Score 2379;  DB 8;  Length 447;
  Best Local Similarity   99.6%;  Pred. No. 4.5e-139;
  Matches  445;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
```

```
RESULT 5
ADS87926
ID   ADS87926 standard; protein; 447 AA.
XX
AC   ADS87926;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 12; SEQ ID NO 19; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             99.3%;  Score 2374;  DB 8;  Length 447;
  Best Local Similarity   99.3%;  Pred. No. 9.2e-139;
  Matches  444;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:||||||||||||||||||| ||||||||||||||
```

```
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 6
ADS94923
ID   ADS94923 standard; protein; 447 AA.
XX
AC   ADS94923;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 14; SEQ ID NO 19; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             99.3%;  Score 2374;  DB 8;  Length 447;
  Best Local Similarity   99.3%;  Pred. No. 9.2e-139;
  Matches  444;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 7
ADS87939
ID   ADS87939 standard; protein; 447 AA.
XX
AC   ADS87939;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
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KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 12; SEQ ID NO 32; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             98.7%;  Score 2360;  DB 8;  Length 447;
  Best Local Similarity   99.1%;  Pred. No. 6.8e-138;
  Matches  443;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||:||||||||||||||| ||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||:|||| ||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 8
ADS94936
ID   ADS94936 standard; protein; 447 AA.
XX
AC   ADS94936;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 14; SEQ ID NO 32; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
```

```
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             98.7%;  Score 2360;  DB 8;  Length 447;
  Best Local Similarity   99.1%;  Pred. No. 6.8e-138;
  Matches  443;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSSAST 120

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447


RESULT 9
ADR46819
ID   ADR46819 standard; protein; 468 AA.
XX
AC   ADR46819;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human antibody B11 heavy chain variable region protein SEQ ID NO:2.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW   CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW   melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW   antibody B11; heavy chain variable region.
XX
OS   Homo sapiens.
XX
PN   WO2004074432-A2.
XX
PD   02-SEP-2004.
XX
PF   30-JAN-2004; 2004WO-US002725.
XX
PR   31-JAN-2003; 2003US-0443979P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T,  Endres M,  He L,  Ramakrishna V;
XX
DR   WPI; 2004-635555/61.
DR   N-PSDB; ADR46818.
XX
PT   New molecular conjugate having a monoclonal antibody that binds to human
PT   APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT   cytotoxic T cell response in cancers and infectious diseases.
XX
PS   Claim 13; SEQ ID NO 2; 82pp; English.
XX
CC   The present invention describes a molecular conjugate comprising a
CC   monoclonal antibody that binds to human antigen presenting cells (APCs)
CC   linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC   comprises a heavy and/or light chain variable region derived from a human
CC   VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC   of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC   described: (1) a molecular conjugate comprising a human antibody heavy
CC   chain and a human antibody light chain, where either or both chains are
CC   linked to betahCG; (2) a molecular conjugate comprising a human single
CC   chain antibody that binds to human APCs linked to betahCG, where the
CC   conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC   (ADR46829); (3) a composition comprising any of the molecular conjugates
CC   as described above, and a carrier, optionally in combination with an
CC   adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC   against betahCG, comprising contacting any of the molecular conjugates
CC   described above with APCs such that the antigen is processed and
CC   presented to T cells in a manner which induces or enhances a T cell-
CC   mediated response against the antigen; (5) immunising a subject
CC   comprising administering any of the molecular conjugates described above,
CC   optionally in combination with an adjuvant, a cytokine which stimulates
CC   proliferation of dendritic cells and/or an immunostimulatory agent; and
CC   (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC   comprising forming a conjugate of the antigen and a monoclonal antibody
CC   which binds to APCs, and contacting the conjugate either in vivo or ex
CC   vivo with APCs such that the antigen is internalised, processed and
CC   presented to T cells in a manner which induces or enhances a cytotoxic T
CC   cell response against the antigen. The molecular conjugate has
CC   cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC   virucide and antimalarial activities, and can be used as a CD8 agonist,
CC   and in vaccines. The methods and compositions of the present invention
CC   are useful for inducing a cytotoxic T cell response, and in particular
CC   for treating autoimmune disorders, cancers and infectious diseases by
CC   eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC   including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC   herpes. The present sequence represents a human antibody B11 heavy chain
CC   variable region, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 468 AA;

  Query Match             95.7%;  Score 2286.5;  DB 8;  Length 468;
  Best Local Similarity   96.6%;  Pred. No. 2.5e-133;
  Matches  432;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||:||||||| :||:|||||||||||||| |||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              ||||||||||||||||||||||||||||||||||  |     | ||:||||||||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDR-GVDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465
```

```
RESULT 10
ADR46827
ID   ADR46827 standard; protein; 613 AA.
XX
AC   ADR46827;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.
XX
KW   molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW   antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW   betahCG; beta chorionic gonadotropin; antibody;
KW   T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW   immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW   CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW   melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW   antibody B11; betahCG-B11 molecular conjugate; fusion protein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004074432-A2.
XX
PD   02-SEP-2004.
XX
PF   30-JAN-2004; 2004WO-US002725.
XX
PR   31-JAN-2003; 2003US-0443979P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T,  Endres M,  He L,  Ramakrishna V;
XX
DR   WPI; 2004-635555/61.
DR   N-PSDB; ADR46826.
XX
PT   New molecular conjugate having a monoclonal antibody that binds to human
PT   APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT   cytotoxic T cell response in cancers and infectious diseases.
XX
PS   Example 1; SEQ ID NO 10; 82pp; English.
XX
CC   The present invention describes a molecular conjugate comprising a
CC   monoclonal antibody that binds to human antigen presenting cells (APCs)
CC   linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC   comprises a heavy and/or light chain variable region derived from a human
CC   VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences
CC   of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC   described: (1) a molecular conjugate comprising a human antibody heavy
CC   chain and a human antibody light chain, where either or both chains are
CC   linked to betahCG; (2) a molecular conjugate comprising a human single
CC   chain antibody that binds to human APCs linked to betahCG, where the
CC   conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC   (ADR46829); (3) a composition comprising any of the molecular conjugates
CC   as described above, and a carrier, optionally in combination with an
CC   adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC   against betahCG, comprising contacting any of the molecular conjugates
CC   described above with APCs such that the antigen is processed and
CC   presented to T cells in a manner which induces or enhances a T cell-
CC   mediated response against the antigen; (5) immunising a subject
CC   comprising administering any of the molecular conjugates described above,
CC   optionally in combination with an adjuvant, a cytokine which stimulates
CC   proliferation of dendritic cells and/or an immunostimulatory agent; and
CC   (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC   comprising forming a conjugate of the antigen and a monoclonal antibody
CC   which binds to APCs, and contacting the conjugate either in vivo or ex
CC   vivo with APCs such that the antigen is internalised, processed and
CC   presented to T cells in a manner which induces or enhances a cytotoxic T
CC   cell response against the antigen. The molecular conjugate has
CC   cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC   virucide and antimalarial activities, and can be used as a CD8 agonist,
CC   and in vaccines. The methods and compositions of the present invention
CC   are useful for inducing a cytotoxic T cell response, and in particular
CC   for treating autoimmune disorders, cancers and infectious diseases by
CC   eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC   including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC   herpes. The present sequence represents a human betahCG-B11 molecular
CC   conjugate, which is used in the exemplification of the present invention.
XX
SQ   Sequence 613 AA;

  Query Match             95.7%;  Score 2286.5;  DB 8;  Length 613;
  Best Local Similarity   96.6%;  Pred. No. 3.4e-133;
  Matches  432;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||| :||:|||||||||||||| |||||||||| |
Db         20 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLEWMGIIYPGDSDTIY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSSAST 120
              |||||||||||||||||||||||||||||||  |    | ||:||||||||||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCTRGDR-GVDYWGQGTLVTVSSAST 138

Qy        121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 198

Qy        181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 258

Qy        241 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 318

Qy        301 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 378

Qy        361 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 438

Qy        421 NVFSCSVMHEALHNHYTQKSLSLSPGK 447
              |||||||||||||||||||||||||||
Db        439 NVFSCSVMHEALHNHYTQKSLSLSPGK 465
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RESULT 11
AAU14177
ID   AAU14177 standard; protein; 474 AA.
XX
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```
AC   AAU14177;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #48.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002623.
XX
PR   25-JAN-2000; 2000US-00491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22482.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage.
XX
PS   Example 4; Page 554-555; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human proteins or
CC   their active domains. The polypeptides, polynucleotides and antibodies
CC   raised against the polypeptides are used in a method of treatment of a
CC   mammal and prevention of disorders caused by the aberrant protein
CC   expression or activity. The polypeptides can be used as molecular weight
CC   markers, food supplements, and in antibody production. The polypeptides
CC   are used to identify compounds which bind to the polypeptides.
CC   Polynucleotides of the invention are used as probes and primers, for
CC   sequencing, for chromosome or gene mapping, in the production of
CC   recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC   therapy. Polypeptides of the invention can be used to target drugs to a
CC   tumour, in assays to determine biological activity, to raise
CC   antibodies/elicit an immune response, to determine quantitative protein
CC   levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
CC   versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
CC   diseases, nervous system disorders, and infection. The present sequence
CC   represents a protein of the invention
XX
SQ   Sequence 474 AA;

  Query Match             95.1%;  Score 2273;  DB 4;  Length 474;
  Best Local Similarity   93.8%;  Pred. No. 1.7e-132;
  Matches  427;  Conservative    9;  Mismatches   11;  Indels    8;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||:|||||||||:|: ||: |||| | |||  ||||||||||||
Db         20 EVQLVQSGAEVKKPGESVKISCKGSGYSFSDYWVAWVRQSPDKGLAWMGIIYPGDSDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSG------SYFYF--DLWGRGTL 112
                ||||||||||||||||||||||||||| |||||||  |      || |:  |:|||||
Db         80 SPSFQGQVTISADKSISTAYLQWSSLKDSDTAMYYCARGARGTAPSYHYYGLDVWGRGTS 139

Qy        113 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199

Qy        173 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 232
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        200 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259

Qy        233 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 319

Qy        293 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 379

Qy        353 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 412
              |||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 439

Qy        413 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||||||||||
Db        440 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474


RESULT 12
ADM41567
ID   ADM41567 standard; protein; 467 AA.
XX
AC   ADM41567;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Anti-interleukin-1 receptor type 1 antibody heavy chain.
XX
KW   Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW   antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW   protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW   analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW   anticonvulsant; dermatological; antigout; antiparkinsonian; antidiabetic;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004022718-A2.
XX
PD   18-MAR-2004.
XX
PF   05-SEP-2003; 2003WO-US027978.
XX
PR   06-SEP-2002; 2002US-0408719P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Varnum B,  Vezina C,  Witte A,  Qian X,  Martin F,  Huang H;
PI   Elliott G;
XX
DR   WPI; 2004-248462/23.
DR   N-PSDB; ADM41566.
XX
PT   Isolated human antibody that specifically binds interleukin-1 receptor
PT   type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
PT   rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
PS   Claim 3; SEQ ID NO 32; 179pp; English.
XX
CC   The present sequence is that of a human anti-interleukin-1 receptor type
CC   1 (IL-1R1) monoclonal antibody (MAb) heavy chain. The invention provides
CC   antibodies that comprise this sequence. Human MAbs to IL-1R1 were
CC   prepared using the HCo7 strain of transgenic mice, which expresses human
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CC   antibody genes. These mice were immunised with purified recombinant IL-
CC   1R1, and splenocytes from immunised mice were fused to a mouse myeloma
CC   cell line to generate hybridomas. Hybridomas which secreted a MAb that
CC   bound with high avidity to IL-1R1 were selected. The MAbs inhibit IL-1
CC   signalling by competing with IL-1beta and IL-1alpha binding to IL-1R.
CC   These MAbs, as well as single chain antibodies single chain Fv
CC   antibodies, Fab antibodies, Fab' antibodies and (Fab')2 antibodies
CC   derived from them, are used in methods of treating IL-1 mediated diseases
CC   or for detecting the amount of IL-1R1 in a sample. IL-1 mediated diseases
CC   include acute pancreatitis, amyotrophic lateral sclerosis, Alzheimer's
CC   disease, cachexia, anorexia, asthma, atherosclerosis, autoimmune
CC   vasculitis, chronic fatigue syndrome, Clostridium associated illnesses,
CC   coronary conditions, cancer including leukaemia and tumour metastasis,
CC   diabetes, endometriosis, fever, fibromyalgia, glomerulonephritis, graft
CC   versus host disease, osteoarthritis, rheumatoid arthritis, inflammatory
CC   eye disease, ischaemia, Kawasaki's disease, learning impairment, lung
CC   diseases, multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's
CC   disease, periodontal disease, pre-term labour, psoriasis, reperfusion
CC   injury, septic shock, side effects of radiation therapy, temporal
CC   mandibular joint disease, sleep disturbance, uveitis, or an inflammatory
CC   condition resulting from strain, sprain, cartilage damage, trauma,
CC   orthopaedic surgery, infection or other disease processes.
XX
SQ   Sequence 467 AA;

  Query Match             94.5%;  Score 2258.5;  DB 8;  Length 467;
  Best Local Similarity   94.9%;  Pred. No. 1.3e-131;
  Matches  425;  Conservative    7;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||:|||||||||||||||||||||:|: :|| |||||||||||| ||||:|| |||||
Db         20 EVQLMQSGAEVKKPGESLKISCKGSGYSFSFHWIAWVRQMPGKGLEWMGIIHPGASDTRY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFYFDLWGRGTLVTVSSAS 119
              |||||||||||| | |  |||||||||||||||:|       ||| ||:||||||||||
Db         80 SPSFQGQVTISADNSNSATYLQWSSLKASDTAMYFCARQRELDYFDYWGQGTLVTVSSAS 139

Qy        120 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL 199

Qy        180 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS 259

Qy        240 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 319

Qy        300 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 379

Qy        360 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 439

Qy        420 GNVFSCSVMHEALHNHYTQKSLSLSPGK 447
              ||||||||||||||||||||||||||||
Db        440 GNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 13
ADS18704
ID   ADS18704 standard; protein; 450 AA.
XX
AC   ADS18704;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Protein sequence of human W17-IgG1 heavy chain.
XX
KW   Antibody; humanised; complementarity determining region; CDR; CDR1; CDR2;
KW   CDR3; W17-IgG1 heavy chain; interleukin -1 beta; IL-1 beta; cytokine;
KW   bone destruction; cartilage destruction; rheumatoid arthritis;
KW   osteoarthritis; clinical efficacy; neuro-inflammation; stroke; ischaemic;
KW   excitotoxic; traumatic head injury; inflammatory disorder; IgG; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "This specification states that there is
FT                   elimination of deamidation at this position, however,
FT                   this residue is a Serine and not an Asparagine or
FT                   Glutamine"
XX
PN   WO2004067568-A2.
XX
PD   12-AUG-2004.
XX
PF   21-JAN-2004; 2004WO-US000019.
XX
PR   24-JAN-2003; 2003US-0442798P.
XX
PA   (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI   Dickinson CD,  Vasserot AP,  Watkins JD,  Lu J;
XX
DR   WPI; 2004-580977/56.
XX
PT   New isolated antibodies that specifically bind mature human IL-1 beta,
PT   useful for treating diseases such as rheumatoid arthritis, osteoarthritis
PT   or neuroinflammation, or for inhibiting cartilage destruction.
XX
PS   Claim 5; SEQ ID NO 47; 79pp; English.
XX
CC   The present invention encompasses humanised IL-1 beta antibodies. These
CC   antibodies are high affinity antibodies with improved stability, reduced
CC   deamidation and highly specific for IL-1 beta compared to the native
CC   antibody. They have potent IL-1 beta neutralising activity. The increased
CC   potency of an existing antibody is achieved through selective changes to
CC   one or more amino acids. The property of the antibodies of the invention
CC   resides primarily in the variable regions or complementarity determining
CC   regions (CDR) of the antibody. The proposed antibodies are comprised of
CC   light chain (CDR1, CDR2 and CDR3) and heavy chain (CDR1, CDR2 and CDR3)
CC   antibody. Interleukin -1 beta is a pro-inflammatory cytokine which is the
CC   primary mediator of bone and cartilage destruction. The over-production
CC   of the IL-1 beta has been implicated in the pathogenesis of a variety of
CC   diseases (rheumatoid arthritis, osteoarthritis, asthma, neuro-
CC   inflammation, graft versus host disease, Crohn's disease, inflammatory
CC   bowel disease, multiple sclerosis, Parkinson's and Alzheimer's disease
CC   etc.). An effective amount of the IL-1 beta antibodies of the present
CC   invention provides clinical efficacy without intolerable side effects or
CC   toxicity. The antibodies are also useful for manufacturing a medicament
CC   for the treatment of rheumatoid arthritis and osteoarthritis. It can be
CC   used to inhibit cartilage destruction and neuro-inflammation (which is
CC   associated with stroke or ischaemic, excitotoxic, or traumatic head
CC   injury). The IL-1 beta antibodies of the invention are preferably used to
CC   treat rheumatoid arthritis (RA), osteoarthritis (OA) and neuro-
CC   inflammation. The IL-1 beta antibodies of the invention can be used alone
CC   or in combination DMARDS (disease modifying antirheumatic drugs) to
CC   reduce IL-1 beta protein levels in plasma. The invention provides the
CC   polynucleotide sequences which encode the antibodies against IL-1 beta.
CC   It also provides the methods for using these antibodies for the treatment
CC   of IL-1 beta related inflammatory disorders. The isolated antibodies of
CC   the invention are selected from the group IgG1 and IgG4. IgG antibodies
CC   are the most abundant immunoglobulin and has the longest half-life in
CC   serum compared to other immunoglobulin. Unlike other immunoglobulins IgG
CC   is efficiently recirculated. The presented protein sequence is the human
CC   W17-IgG1 heavy chain.
XX
SQ   Sequence 450 AA;

  Query Match             91.3%;  Score 2181.5;  DB 8;  Length 450;
  Best Local Similarity   90.9%;  Pred. No. 7.5e-127;
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Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFDRYWIEWVRQAPGQGLEWMGEILPGSGDINY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY---FDLWGRGTLVTVSS 117
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Db         61 NEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARMYYDYDQGFDLWGQGTLVTVSS 120

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Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
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Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360

Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
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Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450
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RESULT 14
ADS18702
ID   ADS18702 standard; protein; 450 AA.
XX
AC   ADS18702;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Protein sequence of human W13-heavy chain.
XX
KW   Antibody; humanised; complementarity determining region; CDR; CDR1; CDR2;
KW   CDR3; W13 heavy chain; interleukin -1 beta; IL-1 beta; cytokine;
KW   bone destruction; cartilage destruction; rheumatoid arthritis;
KW   osteoarthritis; clinical efficacy; neuro-inflammation; stroke; ischaemic;
KW   excitotoxic; traumatic head injury; inflammatory disorder; IgG; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "This specification states that there is
FT                   elimination of deamidation at this position, however,
FT                   this residue is a Serine and not an Asparagine or
FT                   Glutamine"
XX
PN   WO2004067568-A2.
XX
PD   12-AUG-2004.
XX
PF   21-JAN-2004; 2004WO-US000019.
XX
PR   24-JAN-2003; 2003US-0442798P.
XX
PA   (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI   Dickinson CD,  Vasserot AP,  Watkins JD,  Lu J;
XX
DR   WPI; 2004-580977/56.
XX
PT   New isolated antibodies that specifically bind mature human IL-1 beta,
PT   useful for treating diseases such as rheumatoid arthritis, osteoarthritis
PT   or neuroinflammation, or for inhibiting cartilage destruction.
XX
PS   Claim 9; SEQ ID NO 45; 79pp; English.
XX
CC   The present invention encompasses humanised IL-1 beta antibodies. These
CC   antibodies are high affinity antibodies with improved stability, reduced
CC   deamidation and highly specific for IL-1 beta compared to the native
CC   antibody. They have potent IL-1 beta neutralising activity. The increased
CC   potency of an existing antibody is achieved through selective changes to
CC   one or more amino acids. The property of the antibodies of the invention
CC   resides primarily in the variable regions or complementarity determining
CC   regions (CDR) of the antibody. The proposed antibodies are comprised of
CC   light chain (CDR1, CDR2 and CDR3) and heavy chain (CDR1, CDR2 and CDR3)
CC   antibody. Interleukin -1 beta is a pro-inflammatory cytokine which is the
CC   primary mediator of bone and cartilage destruction. The over-production
CC   of the IL-1 beta has been implicated in the pathogenesis of a variety of
CC   diseases (rheumatoid arthritis, osteoarthritis, asthma, neuro-
CC   inflammation, graft versus host disease, Crohn's disease, inflammatory
CC   bowel disease, multiple sclerosis, Parkinson's and Alzheimer's disease
CC   etc.). An effective amount of the IL-1 beta antibodies of the present
CC   invention provides clinical efficacy without intolerable side effects or
CC   toxicity. The antibodies are also useful for manufacturing a medicament
CC   for the treatment of rheumatoid arthritis and osteoarthritis. It can be
CC   used to inhibit cartilage destruction and neuro-inflammation (which is
CC   associated with stroke or ischaemic, excitotoxic, or traumatic head
CC   injury). The IL-1 beta antibodies of the invention are preferably used to
CC   treat rheumatoid arthritis (RA), osteoarthritis (OA) and neuro-
CC   inflammation. The IL-1 beta antibodies of the invention can be used alone
CC   or in combination DMARDS (disease modifying antirheumatic drugs) to
CC   reduce IL-1 beta protein levels in plasma. The invention provides the
CC   polynucleotide sequences which encode the antibodies against IL-1 beta.
CC   It also provides the methods for using these antibodies for the treatment
CC   of IL-1 beta related inflammatory disorders. The isolated antibodies of
CC   the invention are selected from the group IgG1 and IgG4. IgG antibodies
CC   are the most abundant immunoglobulin and has the longest half-life in
CC   serum compared to other immunoglobulin. Unlike other immunoglobulins IgG
CC   is efficiently recirculated. The presented protein sequence is the human
CC   W13-heavy chain.
XX
SQ   Sequence 450 AA;
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  Query Match             91.1%;  Score 2176.5;  DB 8;  Length 450;
  Best Local Similarity   90.7%;  Pred. No. 1.5e-126;
  Matches  408;  Conservative   14;  Mismatches   25;  Indels    3;  Gaps    1;

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              :|||||||||||||| |:|:||| ||| |  ||| |||| ||:||| || | ||  |  |
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFDRYWIEWVRQAPGQGLEWMGEILPGSGDINY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY---FDLWGRGTLVTVSS 117
              :  |:|:|||:|||| ||||:: |||:: |||:|||    | |   || ||:||||||||
Db         61 NEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARMYYDYDQGFDYWGQGTLVTVSS 120

Qy        118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
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Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
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Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
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Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450


RESULT 15
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ID   ADS18708 standard; protein; 450 AA.
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AC   ADS18708;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Protein sequence of human W20-heavy chain.
XX
KW   Antibody; humanised; complementarity determining region; CDR; CDR1; CDR2;
KW   CDR3; W20-heavy chain; interleukin -1 beta; IL-1 beta; cytokine;
KW   bone destruction; cartilage destruction; rheumatoid arthritis;
KW   osteoarthritis; clinical efficacy; neuro-inflammation; stroke; ischaemic;
KW   excitotoxic; traumatic head injury; inflammatory disorder; IgG; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "This specification states that there is
FT                   elimination of deamidation at this position, however,
FT                   this residue is a Serine and not an Asparagine or
FT                   Glutamine"
XX
PN   WO2004067568-A2.
XX
PD   12-AUG-2004.
XX
PF   21-JAN-2004; 2004WO-US000019.
XX
PR   24-JAN-2003; 2003US-0442798P.
XX
PA   (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI   Dickinson CD,  Vasserot AP,  Watkins JD,  Lu J;
XX
DR   WPI; 2004-580977/56.
XX
PT   New isolated antibodies that specifically bind mature human IL-1 beta,
PT   useful for treating diseases such as rheumatoid arthritis, osteoarthritis
PT   or neuroinflammation, or for inhibiting cartilage destruction.
XX
PS   Claim 15; SEQ ID NO 51; 79pp; English.
XX
CC   The present invention encompasses humanised IL-1 beta antibodies. These
CC   antibodies are high affinity antibodies with improved stability, reduced
CC   deamidation and highly specific for IL-1 beta compared to the native
CC   antibody. They have potent IL-1 beta neutralising activity. The increased
CC   potency of an existing antibody is achieved through selective changes to
CC   one or more amino acids. The property of the antibodies of the invention
CC   resides primarily in the variable regions or complementarity determining
CC   regions (CDR) of the antibody. The proposed antibodies are comprised of
CC   light chain (CDR1, CDR2 and CDR3) and heavy chain (CDR1, CDR2 and CDR3)
CC   antibody. Interleukin -1 beta is a pro-inflammatory cytokine which is the
CC   primary mediator of bone and cartilage destruction. The over-production
CC   of the IL-1 beta has been implicated in the pathogenesis of a variety of
CC   diseases (rheumatoid arthritis, osteoarthritis, asthma, neuro-
CC   inflammation, graft versus host disease, Crohn's disease, inflammatory
CC   bowel disease, multiple sclerosis, Parkinson's and Alzheimer's disease
CC   etc.). An effective amount of the IL-1 beta antibodies of the present
CC   invention provides clinical efficacy without intolerable side effects or
CC   toxicity. The antibodies are also useful for manufacturing a medicament
CC   for the treatment of rheumatoid arthritis and osteoarthritis. It can be
CC   used to inhibit cartilage destruction and neuro-inflammation (which is
CC   associated with stroke or ischaemic, excitotoxic, or traumatic head
CC   injury). The IL-1 beta antibodies of the invention are preferably used to
CC   treat rheumatoid arthritis (RA), osteoarthritis (OA) and neuro-
CC   inflammation. The IL-1 beta antibodies of the invention can be used alone
CC   or in combination DMARDS (disease modifying antirheumatic drugs) to
CC   reduce IL-1 beta protein levels in plasma. The invention provides the
CC   polynucleotide sequences which encode the antibodies against IL-1 beta.
CC   It also provides the methods for using these antibodies for the treatment
CC   of IL-1 beta related inflammatory disorders. The isolated antibodies of
CC   the invention are selected from the group IgG1 and IgG4. IgG antibodies
CC   are the most abundant immunoglobulin and has the longest half-life in
CC   serum compared to other immunoglobulin. Unlike other immunoglobulins IgG
CC   is efficiently recirculated. The presented protein sequence is the human
CC   W20-heavy chain.
XX
SQ   Sequence 450 AA;

  Query Match             91.1%;  Score 2176.5;  DB 8;  Length 450;
  Best Local Similarity   90.7%;  Pred. No. 1.5e-126;
  Matches  408;  Conservative   14;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFDRYWIEWVRQAPGQGLEWMGEILPGSGDINY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY---FDLWGRGTLVTVSS 117
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Qy        178 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 237
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Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 297
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Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 357
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Qy        358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
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Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        418 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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(without alignments)
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Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	56	100.0	109	17	US-10-684-957-31	Sequence 31, Appl
3	56	100.0	216	17	US-10-684-957-33	Sequence 33, Appl
4	41	73.2	113	18	US-10-916-840-104	Sequence 104, App
5	41	73.2	226	10	US-09-453-234-80	Sequence 80, Appl
6	39	69.6	10	17	US-10-883-020-24	Sequence 24, Appl
7	39	69.6	104	17	US-10-883-020-34	Sequence 34, Appl
8	38	67.9	131	16	US-10-478-056-27	Sequence 27, Appl
9	38	67.9	2635	18	US-10-840-512-128	Sequence 128, App
10	38	67.9	2644	14	US-10-300-453A-39	Sequence 39, Appl
11	38	67.9	2644	16	US-10-408-765A-184	Sequence 184, App
12	37	66.1	260	15	US-10-369-493-5063	Sequence 5063, Ap
13	37	66.1	532	16	US-10-425-115-299812	Sequence 299812,
14	37	66.1	1431	15	US-10-369-493-6208	Sequence 6208, Ap
15	36	64.3	15	10	US-09-563-222-32	Sequence 32, Appl
16	36	64.3	15	14	US-10-169-351-12	Sequence 12, Appl
17	36	64.3	15	16	US-10-783-950-32	Sequence 32, Appl
18	36	64.3	112	9	US-09-810-502-36	Sequence 36, Appl
19	36	64.3	112	9	US-09-810-502-37	Sequence 37, Appl
20	36	64.3	112	9	US-09-144-886-80	Sequence 80, Appl
21	36	64.3	112	9	US-09-144-886-81	Sequence 81, Appl
22	36	64.3	112	9	US-09-144-886-84	Sequence 84, Appl
23	36	64.3	112	9	US-09-144-886-85	Sequence 85, Appl
24	36	64.3	112	9	US-09-144-886-94	Sequence 94, Appl
25	36	64.3	112	14	US-10-169-351-32	Sequence 32, Appl
26	36	64.3	112	14	US-10-169-351-103	Sequence 103, App
27	36	64.3	112	14	US-10-160-506-81	Sequence 81, Appl
28	36	64.3	112	14	US-10-160-506-82	Sequence 82, Appl
29	36	64.3	112	16	US-10-449-379-81	Sequence 81, Appl
30	36	64.3	112	16	US-10-449-379-82	Sequence 82, Appl
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37	36	64.3	112	16	US-10-160-505-81	Sequence 81, Appl
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40	36	64.3	112	16	US-10-884-133-37	Sequence 37, Appl
41	36	64.3	113	20	US-11-054-539-59	Sequence 59, Appl
42	36	64.3	114	18	US-10-996-316-206	Sequence 206, App
43	36	64.3	117	14	US-10-300-675-42	Sequence 42, Appl
44	36	64.3	131	18	US-10-837-904-33	Sequence 33, Appl
45	36	64.3	136	16	US-10-425-115-333853	Sequence 333853,

ALIGNMENTS

RESULT 1
US-10-684-957-44
; Sequence 44, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-ga
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-44

Query Match 100.0%; Score 56; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 1 QQYGNSFMYT 10

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RESULT 2
US-10-684-957-31
; Sequence 31, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-684-957-31

  Query Match             100.0%;  Score 56;  DB 17;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.022;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||||||||
Db         90 QQYGNSFMYT 99


RESULT 3
US-10-684-957-33
; Sequence 33, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-33

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  Best Local Similarity   100.0%;  Pred. No. 0.045;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||||||||
Db         90 QQYGNSFMYT 99


RESULT 4
US-10-916-840-104
; Sequence 104, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
;  APPLICANT: Hufton, Simon E.
;  APPLICANT:  Hoet, Rene
;  APPLICANT:  Pieters, Henk
;  APPLICANT:  Kent, Rachel Baribault
;  APPLICANT:  Rookey, Kristen
;  TITLE OF INVENTION: TIE1-BINDING LIGANDS
;  FILE REFERENCE: 10280-083001
;  CURRENT APPLICATION NUMBER: US/10/916,840
;  CURRENT FILING DATE:  2004-08-12
;  PRIOR APPLICATION NUMBER: US 60/494,713
;  PRIOR FILING DATE: 2003-08-12
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104
;   LENGTH: 113
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-10-916-840-104

  Query Match             73.2%;  Score 41;  DB 18;  Length 113;
  Best Local Similarity   80.0%;  Pred. No. 12;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||:| |||
Db         94 QQYGSSPMYT 103


RESULT 5
US-09-453-234-80
; Sequence 80, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-20L
US-09-453-234-80

  Query Match             73.2%;  Score 41;  DB 10;  Length 226;
  Best Local Similarity   80.0%;  Pred. No. 24;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||:| |||
Db         90 QQYGSSPMYT 99


RESULT 6
US-10-883-020-24
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; Sequence 24, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:
;  APPLICANT: Ditzel, Henrik
;  APPLICANT:  Jensenius, Jens
;  APPLICANT:  The Scripps Research Institute
;  TITLE OF INVENTION: Cancer-Associated Epitope
;  FILE REFERENCE: 1361.017US1
;  CURRENT APPLICATION NUMBER: US/10/883,020
;  CURRENT FILING DATE:  2004-07-01
;  PRIOR APPLICATION NUMBER: PCT/US03/00297
;  PRIOR FILING DATE: 2003-01-03
;  PRIOR APPLICATION NUMBER: US 60/345,208
;  PRIOR FILING DATE: 2002-01-03
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-883-020-24

  Query Match             69.6%;  Score 39;  DB 17;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 2.3;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||||  ||
Db          1 QQYGNSPPYT 10


RESULT 7
US-10-883-020-34
; Sequence 34, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:
;  APPLICANT: Ditzel, Henrik
;  APPLICANT:  Jensenius, Jens
;  APPLICANT:  The Scripps Research Institute
;  TITLE OF INVENTION: Cancer-Associated Epitope
;  FILE REFERENCE: 1361.017US1
;  CURRENT APPLICATION NUMBER: US/10/883,020
;  CURRENT FILING DATE:  2004-07-01
;  PRIOR APPLICATION NUMBER: PCT/US03/00297
;  PRIOR FILING DATE: 2003-01-03
;  PRIOR APPLICATION NUMBER: US 60/345,208
;  PRIOR FILING DATE: 2002-01-03
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-883-020-34

  Query Match             69.6%;  Score 39;  DB 17;  Length 104;
  Best Local Similarity   80.0%;  Pred. No. 25;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||||  ||
Db         86 QQYGNSPPYT 95


RESULT 8
US-10-478-056-27
; Sequence 27, Application US/10478056
; Publication No. US20040214235A1
; GENERAL INFORMATION:
;  APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;  TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
;  FILE REFERENCE: PH-1573-PCT
;  CURRENT APPLICATION NUMBER: US/10/478,056
;  CURRENT FILING DATE:  2003-11-18
;  PRIOR APPLICATION NUMBER: JP2001-150213
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: JP2001-243040
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: JP2001-314489
;  PRIOR FILING DATE: 2001-10-11
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 131
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-478-056-27

  Query Match             67.9%;  Score 38;  DB 16;  Length 131;
  Best Local Similarity   70.0%;  Pred. No. 47;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||:| :||
Db        110 QQYGSSPLYT 119


RESULT 9
US-10-840-512-128
; Sequence 128, Application US/10840512
; Publication No. US20050125852A1
; GENERAL INFORMATION:
;  APPLICANT: CAENEPEEL, SEAN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  GRIGORIEV, IGOR
;  TITLE OF INVENTION: NOVEL KINASES
;  FILE REFERENCE: 034536-1455
;  CURRENT APPLICATION NUMBER: US/10/840,512
;  CURRENT FILING DATE:  2004-05-07
;  PRIOR APPLICATION NUMBER: 60/469,014
;  PRIOR FILING DATE: 2003-05-09
;  NUMBER OF SEQ ID NOS: 239
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
;   LENGTH: 2635
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-840-512-128

  Query Match             67.9%;  Score 38;  DB 18;  Length 2635;
  Best Local Similarity   75.0%;  Pred. No. 9.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              ||||  |:|
Db       2071 QYGNQFIY 2078


RESULT 10
US-10-300-453A-39
; Sequence 39, Application US/10300453A
; Publication No. US20030165934A1
; GENERAL INFORMATION:
;  APPLICANT: ELLEDGE, STEPHEN J.
;  APPLICANT:  CORTEZ, DAVID K.
;  APPLICANT:  ZOU, LEE
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS IN CHECKPOINT SIGNALING
;  FILE REFERENCE: P02339US
;  CURRENT APPLICATION NUMBER: US/10/300,453A
;  CURRENT FILING DATE:  2003-03-12
;  PRIOR APPLICATION NUMBER: 60/331,821
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
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;   LENGTH: 2644
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-300-453A-39

  Query Match             67.9%;  Score 38;  DB 14;  Length 2644;
  Best Local Similarity   75.0%;  Pred. No. 9.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| |:|
Db       2077 QYGNQFIY 2084


RESULT 11
US-10-408-765A-184
; Sequence 184, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 184
;   LENGTH: 2644
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-184

  Query Match             67.9%;  Score 38;  DB 16;  Length 2644;
  Best Local Similarity   75.0%;  Pred. No. 9.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| |:|
Db       2077 QYGNQFIY 2084


RESULT 12
US-10-369-493-5063
; Sequence 5063, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5063
;   LENGTH: 260
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-10-369-493-5063

  Query Match             66.1%;  Score 37;  DB 15;  Length 260;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMYT 10
              ||||::| |
Db        164 QYGNTYMMT 172


RESULT 13
US-10-425-115-299812
; Sequence 299812, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 299812
;   LENGTH: 532
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(532)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_36498C.1.pep
US-10-425-115-299812

  Query Match             66.1%;  Score 37;  DB 16;  Length 532;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              ||||  |:|
Db         93 QQYGEPFLY 101


RESULT 14
US-10-369-493-6208
; Sequence 6208, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6208
;   LENGTH: 1431
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-10-369-493-6208

  Query Match             66.1%;  Score 37;  DB 15;  Length 1431;
  Best Local Similarity   66.7%;  Pred. No. 8e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMYT 10
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Db       1343 QYGNTYMMT 1351


RESULT 15
US-09-563-222-32
; Sequence 32, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-563-222-32

  Query Match             64.3%;  Score 36;  DB 10;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 12;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db          9 YGNSFMH 15


Search completed: September 11, 2005, 03:14:58
Job time : 122.222 secs
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:45:00 ; Search time 33.3333 Seconds
(without alignments)
22.395 Million cell updates/sec

Title: US-10-684-957-44
Perfect score: 56
Sequence: 1 QQYGNSFMYT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	73.2	226	4	US-09-456-090A-80	Sequence 80, Appl
2	41	73.2	226	4	US-09-453-234-80	Sequence 80, Appl
3	38	67.9	500	1	US-08-117-083-69	Sequence 69, Appl
4	38	67.9	2644	4	US-09-029-047C-2	Sequence 2, Appli
5	37	66.1	134	1	US-08-405-034-4	Sequence 4, Appli
6	36	64.3	15	4	US-09-563-222C-32	Sequence 32, Appl
7	36	64.3	91	2	US-08-273-146-49	Sequence 49, Appl
8	36	64.3	111	1	US-08-111-080-30	Sequence 30, Appl
9	36	64.3	111	1	US-08-111-080-32	Sequence 32, Appl
10	36	64.3	111	1	US-08-275-053-11	Sequence 11, Appl
11	36	64.3	111	1	US-08-275-053-14	Sequence 14, Appl
12	36	64.3	111	1	US-08-211-980-30	Sequence 30, Appl
13	36	64.3	111	1	US-08-211-980-32	Sequence 32, Appl
14	36	64.3	111	5	PCT-US93-07967-30	Sequence 30, Appl
15	36	64.3	111	5	PCT-US93-07967-32	Sequence 32, Appl
16	36	64.3	112	4	US-09-810-502-36	Sequence 36, Appl
17	36	64.3	112	4	US-09-810-502-37	Sequence 37, Appl
18	36	64.3	121	1	US-08-111-080-18	Sequence 18, Appl
19	36	64.3	121	1	US-08-111-080-22	Sequence 22, Appl
20	36	64.3	121	1	US-08-211-980-18	Sequence 18, Appl
21	36	64.3	121	1	US-08-211-980-22	Sequence 22, Appl
22	36	64.3	121	5	PCT-US92-07111-17	Sequence 17, Appl
23	36	64.3	121	5	PCT-US93-07967-18	Sequence 18, Appl
24	36	64.3	121	5	PCT-US93-07967-22	Sequence 22, Appl
25	36	64.3	131	1	US-08-137-117D-33	Sequence 33, Appl
26	36	64.3	131	2	US-08-436-717-33	Sequence 33, Appl
27	36	64.3	131	2	US-08-621-751A-10	Sequence 10, Appl
28	36	64.3	131	2	US-08-621-751A-14	Sequence 14, Appl
29	36	64.3	215	4	US-09-724-623-95	Sequence 95, Appl
30	36	64.3	224	4	US-09-456-090A-52	Sequence 52, Appl
31	36	64.3	224	4	US-09-456-090A-76	Sequence 76, Appl
32	36	64.3	224	4	US-09-453-234-52	Sequence 52, Appl
33	36	64.3	224	4	US-09-453-234-76	Sequence 76, Appl
34	36	64.3	239	4	US-09-248-796A-19899	Sequence 19899, A
35	35.5	63.4	104	1	US-08-276-852-100	Sequence 100, App
36	35.5	63.4	104	1	US-08-899-575-100	Sequence 100, App
37	35.5	63.4	104	1	US-08-899-575-100	Sequence 100, App
38	35.5	63.4	104	5	PCT-US95-08743-100	Sequence 100, App
39	35	62.5	100	1	US-08-307-499-3	Sequence 3, Appli
40	35	62.5	100	3	US-09-299-268-3	Sequence 3, Appli
41	35	62.5	139	2	US-08-894-922A-5	Sequence 5, Appli
42	35	62.5	252	2	US-08-894-922A-14	Sequence 14, Appl
43	35	62.5	271	2	US-08-894-922A-10	Sequence 10, Appl
44	35	62.5	311	4	US-09-134-000C-3973	Sequence 3973, Ap
45	35	62.5	313	4	US-09-270-767-36171	Sequence 36171, A

ALIGNMENTS

RESULT 1
US-09-456-090A-80
; Sequence 80, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-20L
US-09-456-090A-80

Query Match 73.2%; Score 41; DB 4; Length 226;
Best Local Similarity 80.0%; Pred. No. 8.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYGNSFMYT 10
              ||||:| |||
Db         90 QQYGSSPMYT 99
```

RESULT 2
US-09-453-234-80
; Sequence 80, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 80
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-20L
US-09-453-234-80

  Query Match             73.2%;  Score 41;  DB 4;  Length 226;
  Best Local Similarity   80.0%;  Pred. No. 8.2;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||:| |||
Db         90 QQYGSSPMYT 99


RESULT 3
US-08-117-083-69
; Sequence 69, Application US/08117083
; Patent No. 5719054
;  GENERAL INFORMATION:
;    APPLICANT:  Boursnell, Michael E.
;    APPLICANT:  Inglis, Stephen C.
;    APPLICANT:  Munro, Alan J.
;    TITLE OF INVENTION:  Recombinant Virus Vectors Encoding Human
;    TITLE OF INVENTION:  Papilloma Virus Proteins
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Walter H. Dreger
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/117,083
;      FILING DATE:  10-SEP-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-58783
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  500 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..500
;      OTHER INFORMATION:  /note= "Xaa refers to stop codon in
;      OTHER INFORMATION:  the open reading frame."
US-08-117-083-69

  Query Match             67.9%;  Score 38;  DB 1;  Length 500;
  Best Local Similarity   75.0%;  Pred. No. 62;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMYT 10
              ||:||:||
Db        154 YGSSFLYT 161


RESULT 4
US-09-029-047C-2
; Sequence 2, Application US/09029047C
; Patent No. 6632936
; GENERAL INFORMATION:
;  APPLICANT: Carr, Antony M.
;  TITLE OF INVENTION: Cell-Cycle Checkpoint Genes
;  FILE REFERENCE: 27866/34132
;  CURRENT APPLICATION NUMBER: US/09/029,047C
;  CURRENT FILING DATE:  1999-05-11
;  PRIOR APPLICATION NUMBER: PCT/GB96/02197
;  PRIOR FILING DATE: 1996-09-06
;  PRIOR APPLICATION NUMBER: GB 9518220.0
;  PRIOR FILING DATE: 1995-09-06
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
;   LENGTH: 2644
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-029-047C-2

  Query Match             67.9%;  Score 38;  DB 4;  Length 2644;
  Best Local Similarity   75.0%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| |:|
Db       2077 QYGNQFIY 2084


RESULT 5
US-08-405-034-4
; Sequence 4, Application US/08405034
; Patent No. 5744585
; Patent No. 5744585 5712371
;  GENERAL INFORMATION:
;    APPLICANT:  Medenica, Rajko D.
;    APPLICANT:  Mukerjee, Sonjoy
;    TITLE OF INVENTION:  Human Monoclonal Antibody Against Lung
;    TITLE OF INVENTION:  Carcinoma
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DeWitt Ross & Stevens, S.C.
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/405,034
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sara, Charles S.
;      REGISTRATION NUMBER:  30,492
;      REFERENCE/DOCKET NUMBER:  34656.009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-831-2100
;      TELEFAX:  608-831-2106
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  134 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-405-034-4
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  Query Match             66.1%;  Score 37;  DB 1;  Length 134;
  Best Local Similarity   70.0%;  Pred. No. 25;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||:|  ||
Db        110 QQYGSSARYT 119


RESULT 6
US-09-563-222C-32
; Sequence 32, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
;  APPLICANT: EPICYTE PHARMACEUTICALS, INC.
;  APPLICANT:  HIATT, ANDREW C.
;  APPLICANT:  HEIN, MICH B.
;  TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
;  FILE REFERENCE: 068904-0501
;  CURRENT APPLICATION NUMBER: US/09/563,222C
;  CURRENT FILING DATE:  2000-05-02
;  PRIOR APPLICATION NUMBER: PCT/US01/14349
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 09/563,222
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-563-222C-32

  Query Match             64.3%;  Score 36;  DB 4;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 4.1;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db          9 YGNSFMH 15


RESULT 7
US-08-273-146-49
; Sequence 49, Application US/08273146
; Patent No. 5855885
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Rodger
;    APPLICANT:  McCafferty, John
;    APPLICANT:  Chiswell, David
;    APPLICANT:  Darsley, Michael J.
;    APPLICANT:  Fitzgerald, Kevin
;    APPLICANT:  Kenten, John H.
;    APPLICANT:  Martin, Mark T.
;    APPLICANT:  Titmas, Richard C.
;    APPLICANT:  Williams, Richard O.
;    TITLE OF INVENTION:  The Isolation and Production of
;    TITLE OF INVENTION:  Catalytic Antibodies using Phage Technology
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IGEN, Inc.
;      STREET:  1530 East Jefferson St.
;      CITY:  Rockville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20852
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/273,146
;      FILING DATE:  14-JUL-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ryan, John W.
;      REGISTRATION NUMBER:  33,771
;      REFERENCE/DOCKET NUMBER:  09000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-984-8000
;      TELEFAX:  301-230-0158
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  91 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-273-146-49

  Query Match             64.3%;  Score 36;  DB 2;  Length 91;
  Best Local Similarity   85.7%;  Pred. No. 25;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         24 YGNSFMH 30


RESULT 8
US-08-111-080-30
; Sequence 30, Application 08/111080
; Patent No. 5558865
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    TITLE OF INVENTION:  HIV Immunotherapeutics
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  08/111,080
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/748,562
;      FILING DATE:  22-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07111
;      FILING DATE:  24-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,457
;      FILING DATE:  22-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25,447
;      REFERENCE/DOCKET NUMBER:  31629
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-111-080-30

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 9
US-08-111-080-32
; Sequence 32, Application 08/111080
; Patent No. 5558865
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    TITLE OF INVENTION:  HIV Immunotherapeutics
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  08/111,080
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/748,562
;      FILING DATE:  22-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07111
;      FILING DATE:  24-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,457
;      FILING DATE:  22-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25,447
;      REFERENCE/DOCKET NUMBER:  31629
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-111-080-32

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 10
US-08-275-053-11
; Sequence 11, Application US/08275053
; Patent No. 5607847
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant human anti-human immunodeficiency
;    TITLE OF INVENTION:  virus antibody.
;    NUMBER OF SEQUENCES:  16
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/275,053
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/01798
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-275-053-11

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 11
US-08-275-053-14
; Sequence 14, Application US/08275053
; Patent No. 5607847
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant human anti-human immunodeficiency
;    TITLE OF INVENTION:  virus antibody.
;    NUMBER OF SEQUENCES:  16
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/275,053
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/01798
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-275-053-14

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 12
US-08-211-980-30
; Sequence 30, Application US/08211980
```

```
; Patent No. 5665569
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    TITLE OF INVENTION:  HIV Immunotherapeutics
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,980
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07111
;      FILING DATE:  24-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,457
;      FILING DATE:  22-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25,447
;      REFERENCE/DOCKET NUMBER:  31629
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-211-980-30

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 13
US-08-211-980-32
; Sequence 32, Application US/08211980
; Patent No. 5665569
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    TITLE OF INVENTION:  HIV Immunotherapeutics
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,980
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07111
;      FILING DATE:  24-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,457
;      FILING DATE:  22-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25,447
;      REFERENCE/DOCKET NUMBER:  31629
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-211-980-32

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 14
PCT-US93-07967-30
; Sequence 30, Application PC/TUS9307967
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    TITLE OF INVENTION:  HIV Immunotherapeutics
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07967
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07111
;      FILING DATE:  24-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,457
;      FILING DATE:  22-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25,447
;      REFERENCE/DOCKET NUMBER:  31629
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
```

```
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US93-07967-30

  Query Match             64.3%;  Score 36;  DB 5;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              |||||:
Db         32 YGNSFMH 38


RESULT 15
PCT-US93-07967-32
; Sequence 32, Application PC/TUS9307967
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    TITLE OF INVENTION:  HIV Immunotherapeutics
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07967
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07111
;      FILING DATE:  24-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,457
;      FILING DATE:  22-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25,447
;      REFERENCE/DOCKET NUMBER:  31629
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US93-07967-32

  Query Match             64.3%;  Score 36;  DB 5;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              |||||:
Db         32 YGNSFMH 38
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Search completed: September 11, 2005, 02:57:38
Job time : 34.3333 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:43:25 ; Search time 125.556 Seconds
(without alignments)
40.785 Million cell updates/sec

Title: US-10-684-957-44
Perfect score: 56
Sequence: 1 QQYGNSFMYT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	78.6	374	2	Q91XV0	Q91xv0 rattus norv
2	44	78.6	654	2	Q91XV2	Q91xv2 rattus norv
3	44	78.6	708	2	Q91XV1	Q91xv1 rattus norv
4	39	69.6	293	2	Q8UBJ3	Q8ubj3 agrobacteri
5	39	69.6	1105	2	Q7QAM0	Q7qam0 anopheles g
6	39	69.6	1427	1	DPO3_CLOTE	Q895k2 clostridium
7	38	67.9	60	2	Q8VB98	Q8vb98 white spot
8	38	67.9	281	2	Q7UCD2	Q7ucd2 shigella fl
9	38	67.9	340	2	Q8X8W9	Q8x8w9 escherichia
10	38	67.9	341	2	Q83R18	Q83r18 shigella fl
11	38	67.9	2644	2	Q13535	Q13535 homo sapien
12	38	67.9	2644	2	Q7KYL3	Q7kyl3 homo sapien
13	38	67.9	3207	2	Q8IHQ0	Q8ihq0 plasmodium
14	37	66.1	260	2	O01842	O01842 caenorhabdi
15	37	66.1	597	1	ETFD_CAEEL	Q11190 c probable
16	37	66.1	902	2	Q8A5V3	Q8a5v3 bacteroides
17	37	66.1	1288	2	Q753D4	Q753d4 ashbya goss
18	37	66.1	1431	2	Q9XUD4	Q9xud4 caenorhabdi
19	37	66.1	1564	2	Q9XW49	Q9xw49 caenorhabdi
20	36	64.3	47	2	Q70UC9	Q70uc9 mycena croc
21	36	64.3	47	2	Q70UH9	Q70uh9 uncultured
22	36	64.3	87	2	Q81HI6	Q81hi6 bacillus ce
23	36	64.3	91	2	Q63FK6	Q63fk6 bacillus ce
24	36	64.3	91	2	Q81UQ9	Q81uq9 bacillus an
25	36	64.3	91	2	Q6HN12	Q6hn12 bacillus th
26	36	64.3	111	1	KV3H_MOUSE	P01660 mus musculu
27	36	64.3	111	1	KV3J_MOUSE	P01662 mus musculu
28	36	64.3	111	1	KV3K_MOUSE	P01663 mus musculu
29	36	64.3	131	1	KV3I_MOUSE	P01661 mus musculu
30	36	64.3	137	2	Q8PU27	Q8pu27 methanosarc
31	36	64.3	207	2	Q997G7	Q997g7 bovine aden
32	36	64.3	230	2	Q6UD04	Q6ud04 uncultured
33	36	64.3	230	2	Q6UD32	Q6ud32 uncultured
34	36	64.3	276	2	Q8Y834	Q8y834 listeria mo
35	36	64.3	281	2	Q7TV60	Q7tv60 prochloroco
36	36	64.3	283	2	Q65D18	Q65d18 bacillus li
37	36	64.3	283	2	P96585	P96585 bacillus su
38	36	64.3	304	2	Q9UZU9	Q9uzu9 pyrococcus
39	36	64.3	317	2	O57912	O57912 pyrococcus
40	36	64.3	414	2	Q9C8K4	Q9c8k4 arabidopsis
41	36	64.3	540	2	Q6C8P9	Q6c8p9 yarrowia li
42	36	64.3	558	1	YCXA_ASTLO	P34782 astasia lon
43	36	64.3	579	2	O60950	O60950 dictyosteli
44	36	64.3	681	2	Q6CMS3	Q6cms3 kluyveromyc
45	36	64.3	806	2	Q9DDL2	Q9ddl2 brachydanio

ALIGNMENTS

RESULT 1
Q91XV0
ID Q91XV0 PRELIMINARY; PRT; 374 AA.
AC Q91XV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gonadotropin inducible ovarian transcription factor 2 beta.
GN Name=GIOT2 beta;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=21463416; PubMed=11579202; DOI=10.1210/me.15.10.1693;
RA Mizutani T., Yamada K., Yazawa T., Okada T., Minegishi T.,
RA Miyamoto K.;
RT "Cloning and Characterization of Gonadotropin-Inducible Ovarian
RT Transcription Factors (GIOT1 and -2) That Are Novel Members of the
RT (Cys)2-(His)2-Type Zinc Finger Protein Family.";
RL Mol. Endocrinol. 15:1693-1705(2001).
DR EMBL; AB047638; BAB63448.1; -.
DR HSSP; P08047; 1SP2.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR Pfam; PF00096; zf-C2H2; 6.
DR ProDom; PD000003; Znf_C2H2; 5.
DR SMART; SM00355; ZnF_C2H2; 6.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
SQ SEQUENCE 374 AA; 43626 MW; 9E9FBFECC89BA88E CRC64;

Query Match 78.6%; Score 44; DB 2; Length 374;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QQYGNSFMY 9
              |:||||:|
Db        100 QEYGNSFVY 108
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RESULT 2
Q91XV2
ID Q91XV2 PRELIMINARY; PRT; 654 AA.
AC Q91XV2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gonadotropin inducible ovarian transcription factor 1.
GN Name=GIOT1;
OS Rattus norvegicus (Rat).

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=21463416; PubMed=11579202; DOI=10.1210/me.15.10.1693;
RA   Mizutani T., Yamada K., Yazawa T., Okada T., Minegishi T.,
RA   Miyamoto K.;
RT   "Cloning and Characterization of Gonadotropin-Inducible Ovarian
RT   Transcription Factors (GIOT1 and -2) That Are Novel Members of the
RT   (Cys)2-(His)2-Type Zinc Finger Protein Family.";
RL   Mol. Endocrinol. 15:1693-1705(2001).
DR   EMBL; AB047636; BAB63446.1; -.
DR   HSSP; P08047; 1SP2.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF01352; KRAB; 1.
DR   Pfam; PF00096; zf-C2H2; 14.
DR   PRINTS; PR00048; ZINCFINGER.
DR   ProDom; PD000003; Znf_C2H2; 14.
DR   SMART; SM00349; KRAB; 1.
DR   SMART; SM00355; ZnF_C2H2; 15.
DR   PROSITE; PS50805; KRAB; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 14.
SQ   SEQUENCE   654 AA;  76008 MW;  90EFD9E560FBD9DC CRC64;

  Query Match             78.6%;  Score 44;  DB 2;  Length 654;
  Best Local Similarity   77.8%;  Pred. No. 7.7;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              |:|||||:|
Db        132 QEYGNSFVY 140


RESULT 3
Q91XV1
ID   Q91XV1      PRELIMINARY;      PRT;   708 AA.
AC   Q91XV1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Gonadotropin inducible ovarian transcription factor 2 alpha.
GN   Name=GIOT2 alpha;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=21463416; PubMed=11579202; DOI=10.1210/me.15.10.1693;
RA   Mizutani T., Yamada K., Yazawa T., Okada T., Minegishi T.,
RA   Miyamoto K.;
RT   "Cloning and Characterization of Gonadotropin-Inducible Ovarian
RT   Transcription Factors (GIOT1 and -2) That Are Novel Members of the
RT   (Cys)2-(His)2-Type Zinc Finger Protein Family.";
RL   Mol. Endocrinol. 15:1693-1705(2001).
DR   EMBL; AB047637; BAB63447.1; -.
DR   HSSP; P08047; 1SP2.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   Pfam; PF00096; zf-C2H2; 17.
DR   PRINTS; PR00048; ZINCFINGER.
DR   ProDom; PD000003; Znf_C2H2; 15.
DR   SMART; SM00355; ZnF_C2H2; 18.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 17.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 19.
SQ   SEQUENCE   708 AA;  82154 MW;  3BB14243B8A7F439 CRC64;

  Query Match             78.6%;  Score 44;  DB 2;  Length 708;
  Best Local Similarity   77.8%;  Pred. No. 8.3;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              |:|||||:|
Db        100 QEYGNSFVY 108


RESULT 4
Q8UBJ3
ID   Q8UBJ3      PRELIMINARY;      PRT;   293 AA.
AC   Q8UBJ3; Q7CRD9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   ABC transporter, membrane spanning protein (AGR_L_3561p).
GN   OrderedLocusNames=AGR_L_3561, Atu3023;
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dupont;
RX   MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Cereon;
RX   MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
CC   -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC       Probably responsible for the translocation of the substrate across
CC       the membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC       system permease family.
DR   EMBL; AE009232; AAL43839.1; -.
DR   EMBL; AE008382; AAK90360.1; -.
DR   PIR; AI2927; AI2927.
DR   PIR; F98354; F98354.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp_1; 1.
DR   PROSITE; PS50928; ABC_TM1; 1.
KW   Transmembrane; Transport; Complete proteome.
SQ   SEQUENCE   293 AA;  32873 MW;  90EF9A5989D8C59D CRC64;
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  Query Match             69.6%;  Score 39;  DB 2;  Length 293;
  Best Local Similarity   75.0%;  Pred. No. 32;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMYT 10
              |||:|:||
Db         77 YGNTFIYT 84


RESULT 5
Q7QAM0
ID   Q7QAM0      PRELIMINARY;      PRT;  1105 AA.
AC   Q7QAM0;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP7789 (Fragment).
GN   Name=agCG53371; ORFNames=ENSANGG00000008883;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008888; EAA08804.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   1105 AA;  121512 MW;  8ECEB658C6D06195 CRC64;

  Query Match             69.6%;  Score 39;  DB 2;  Length 1105;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              ||:|| :||
Db       1069 QQFGNPYMY 1077


RESULT 6
DPO3_CLOTE
ID   DPO3_CLOTE     STANDARD;      PRT;  1427 AA.
AC   Q895K2;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
GN   Name=polC; OrderedLocusNames=CTC01271;
OS   Clostridium tetani.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Massachusetts / E88;
RX   MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA   Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
RA   Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA   Gottschalk G.;
RT   "The genome sequence of Clostridium tetani, the causative agent of
RT   tetanus disease.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
CC   -!- FUNCTION: Required for replicative DNA synthesis. This DNA
CC       polymerase also exhibits 3' to 5' exonuclease activity (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + {DNA}(N).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the DNA polymerase type-C family. PolC
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE015940; AAO35838.1; -.
DR   HAMAP; MF_00356; -; 1.
DR   InterPro; IPR006054; DnaQ.
DR   InterPro; IPR006055; Exonuclease.
DR   InterPro; IPR008994; Nucleic_acid_OB.
DR   InterPro; IPR003141; Pesterase_PHP_N.
DR   InterPro; IPR004013; PHP_C.
DR   InterPro; IPR006308; PolC_gram_pos.
DR   InterPro; IPR004365; tRNA_anti.
DR   Pfam; PF00929; Exonuc_X-T; 1.
DR   Pfam; PF02811; PHP_C; 1.
DR   Pfam; PF02231; PHP_N; 1.
DR   Pfam; PF01336; tRNA_anti; 1.
DR   SMART; SM00479; EXOIII; 1.
DR   SMART; SM00481; POLIIIAc; 1.
KW   Complete proteome; DNA replication; DNA-directed DNA polymerase;
KW   Exonuclease; Hydrolase; Nuclease; Transferase.
FT   DOMAIN      413    576       Exonuclease.
SQ   SEQUENCE   1427 AA;  162359 MW;  23D6582BF9FAD4CD CRC64;

  Query Match             69.6%;  Score 39;  DB 1;  Length 1427;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| |:|
Db        121 QYGNDFLY 128


RESULT 7
Q8VB98
ID   Q8VB98      PRELIMINARY;      PRT;    60 AA.
AC   Q8VB98;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Wsv082 (WSSV139).
OS   White spot syndrome virus (WSSV).
OC   Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX   NCBI_TaxID=92652;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21548311; PubMed=11689662;
RX   DOI=10.1128/JVI.75.23.11811-11820.2001;
RA   Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT   "Complete genome sequence of the shrimp white spot bacilliform
RT   virus.";
RL   J. Virol. 75:11811-11820(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
RA   Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
RA   Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT   "Identification and characterization of a shrimp white spot syndrome
RT   virus (WSSV) gene that encodes a novel chimeric polypeptide of
RT   cellular-type thymidine kinase and thymidylate kinase.";
RL   Virology 277:100-110(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
RA   Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA   Lo C.F., Kou G.H.;
RT   "Identification of a nucleocapsid protein (VP35) gene of shrimp white
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RT   spot syndrome virus and characterization of the motif important for
RT   targeting VP35 to the nuclei of transfected insect cells.";
RL   Virology 293:44-53(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Lo C.-F., Kou G.-H.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332093; AAL33086.1; -.
DR   EMBL; AF440570; AAL89007.1; -.
SQ   SEQUENCE   60 AA;  6872 MW;  93D24C3EE2818AF4 CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 60;
  Best Local Similarity   66.7%;  Pred. No. 10;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              |:| |||:|
Db         29 QRYSNSFLY 37


RESULT 8
Q7UCD2
ID   Q7UCD2      PRELIMINARY;      PRT;   281 AA.
AC   Q7UCD2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative integrase for prophage CP-933U.
GN   OrderedLocusNames=S2146;
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2457T;
RX   MEDLINE=22590274; PubMed=12704152;
RX   DOI=10.1128/IAI.71.5.2775-2786.2003;
RA   Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA   Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA   Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA   Schwartz D.C., Blattner F.R.;
RT   "Complete genome sequence and comparative genomics of Shigella
RT   flexneri serotype 2a strain 2457T.";
RL   Infect. Immun. 71:2775-2786(2003).
DR   EMBL; AE016985; AAP17412.1; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0015074; P:DNA integration; IEA.
DR   GO; GO:0006310; P:DNA recombination; IEA.
DR   InterPro; IPR011010; DNA_brk_join_enz.
DR   InterPro; IPR010998; L_intgrse_like_N.
DR   InterPro; IPR002104; Phage_integrase.
DR   InterPro; IPR004107; Phage_integr_N.
DR   Pfam; PF00589; Phage_integrase; 1.
DR   Pfam; PF02899; Phage_integr_N; 1.
SQ   SEQUENCE   281 AA;  32187 MW;  11677C16808DA481 CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 281;
  Best Local Similarity   75.0%;  Pred. No. 48;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db        191 QYGNRYMY 198


RESULT 9
Q8X8W9
ID   Q8X8W9      PRELIMINARY;      PRT;   340 AA.
AC   Q8X8W9; Q7ACT4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative integrase.
GN   Name=intU; OrderedLocusNames=ECs2773, z3130;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927 /  EHEC;
RX   MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AE005423; AAG57039.1; -.
DR   EMBL; AP002559; BAB36196.1; -.
DR   PIR; C85822; C85822.
DR   PIR; E90975; E90975.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0015074; P:DNA integration; IEA.
DR   GO; GO:0006310; P:DNA recombination; IEA.
DR   InterPro; IPR011010; DNA_brk_join_enz.
DR   InterPro; IPR010998; L_intgrse_like_N.
DR   InterPro; IPR002104; Phage_integrase.
DR   InterPro; IPR004107; Phage_integr_N.
DR   Pfam; PF00589; Phage_integrase; 1.
DR   Pfam; PF02899; Phage_integr_N; 1.
KW   Complete proteome.
SQ   SEQUENCE   340 AA;  39145 MW;  9585A481446B4B03 CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 340;
  Best Local Similarity   75.0%;  Pred. No. 58;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db        250 QYGNRYMY 257


RESULT 10
Q83R18
ID   Q83R18      PRELIMINARY;      PRT;   341 AA.
AC   Q83R18;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative integrase for prophage CP-933U.
GN   Name=intU; OrderedLocusNames=SF2044;
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=301 / Serotype 2a;
RX   MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA   Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
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RA   Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA   Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA   Yu J.;
RT   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT   through comparison with genomes of Escherichia coli K12 and O157.";
RL   Nucleic Acids Res. 30:4432-4441(2002).
DR   EMBL; AE015221; AAN43587.1; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0015074; P:DNA integration; IEA.
DR   GO; GO:0006310; P:DNA recombination; IEA.
DR   InterPro; IPR011010; DNA_brk_join_enz.
DR   InterPro; IPR010998; L_intgrse_like_N.
DR   InterPro; IPR002104; Phage_integrase.
DR   InterPro; IPR004107; Phage_integr_N.
DR   Pfam; PF00589; Phage_integrase; 1.
DR   Pfam; PF02899; Phage_integr_N; 1.
KW   Complete proteome.
SQ   SEQUENCE   341 AA;  39273 MW;  6D5AAB8EFAC91E3D CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 341;
  Best Local Similarity   75.0%;  Pred. No. 58;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db        251 QYGNRYMY 258


RESULT 11
Q13535
ID   Q13535      PRELIMINARY;      PRT;  2644 AA.
AC   Q13535; Q93051;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   FRAP-related protein.
GN   Name=FRP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96181495; PubMed=8610130; DOI=10.1073/pnas.93.7.2850;
RA   Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L.;
RT   "cDNA cloning and gene mapping of a candidate human cell cycle
RT   checkpoint protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:2850-2855(1996).
DR   EMBL; U49844; AAC50405.1; -.
DR   Genew; HGNC:882; ATR.
DR   GO; GO:0004672; F:protein kinase activity; TAS.
DR   GO; GO:0007049; P:cell cycle; TAS.
DR   GO; GO:0000075; P:cell cycle checkpoint; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006281; P:DNA repair; TAS.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR003152; FATC.
DR   InterPro; IPR009050; Globin_like.
DR   InterPro; IPR000357; HEAT.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR008941; TPR-like.
DR   Pfam; PF02260; FATC; 1.
DR   Pfam; PF02985; HEAT; 2.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS50077; HEAT_REPEAT; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
SQ   SEQUENCE   2644 AA;  301364 MW;  11BC22297FB9A802 CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 2644;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db       2077 QYGNQFIY 2084


RESULT 12
Q7KYL3
ID   Q7KYL3      PRELIMINARY;      PRT;  2644 AA.
AC   Q7KYL3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Protein kinase ATR.
GN   Name=atr;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97133293; PubMed=8978690;
RA   Bentley N.J., Holtzman D.A., Flaggs G., Keegan K.S., DeMaggio A.,
RA   Ford J.C., Hoekstra M., Carr A.M.;
RT   "The Schizosaccharomyces pombe rad3 checkpoint gene.";
RL   EMBO J. 15:6641-6651(1996).
DR   EMBL; Y09077; CAA70298.1; -.
DR   EMBL; U76308; AAC50929.1; -.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR003152; FATC.
DR   InterPro; IPR000357; HEAT.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR008941; TPR-like.
DR   Pfam; PF02260; FATC; 1.
DR   Pfam; PF02985; HEAT; 2.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS50077; HEAT_REPEAT; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
SQ   SEQUENCE   2644 AA;  301449 MW;  3889CAB9330E630A CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 2644;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db       2077 QYGNQFIY 2084


RESULT 13
Q8IHQ0
ID   Q8IHQ0      PRELIMINARY;      PRT;  3207 AA.
AC   Q8IHQ0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=PF11_0479;
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA   Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA   Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
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RA   Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA   Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
RA   Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA   Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA   McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA   Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA   Fraser C.M., Barrell B.;
RT   "Genome sequence of the human malaria parasite Plasmodium
RT   falciparum.";
RL   Nature 419:498-511(2002).
DR   EMBL; AE014843; AAN36059.1; -.
DR   InterPro; IPR006162; Ppantne_S.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   3207 AA;  377919 MW;  71C32BF88BF06A59 CRC64;

  Query Match             67.9%;  Score 38;  DB 2;  Length 3207;
  Best Local Similarity   70.0%;  Pred. No. 5.6e+02;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||| | | ||
Db       2063 QQYTNGFCYT 2072


RESULT 14
O01842
ID   O01842      PRELIMINARY;      PRT;   260 AA.
AC   O01842;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein F56F4.6.
GN   Name=F56F4.6; ORFNames=F56F4.6;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   WormBase Consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Murray J., Wohldmann P., Gillam B.;
RT   "The sequence of C. elegans cosmid F56F4.";
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RG   WormBase Consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AF003146; AAB54203.1; -.
DR   PIR; T15237; T15237.
DR   WormBase; WBGene00018982; F56F4.6.
DR   WormPep; F56F4.6; CE11270.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Hypothetical protein.
SQ   SEQUENCE   260 AA;  28525 MW;  75D5438F79BD44CC CRC64;

  Query Match             66.1%;  Score 37;  DB 2;  Length 260;
  Best Local Similarity   66.7%;  Pred. No. 69;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMYT 10
              ||||::| |
Db        164 QYGNTYMMT 172


RESULT 15
ETFD_CAEEL
ID   ETFD_CAEEL     STANDARD;      PRT;   597 AA.
AC   Q11190;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable electron transfer flavoprotein-ubiquinone oxidoreductase,
DE   mitochondrial precursor (EC 1.5.5.1) (ETF-QO) (ETF-ubiquinone
DE   oxidoreductase) (ETF dehydrogenase) (Electron-transferring-
DE   flavoprotein dehydrogenase) (Lethal protein 721).
GN   Name=let-721; ORFNames=C05D11.12;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   REVISIONS.
RA   Waterston R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Accepts electrons from ETF and reduces ubiquinone (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Reduced electron-transferring flavoprotein +
CC       ubiquinone = electron-transferring flavoprotein + ubiquinol.
CC   -!- COFACTOR: FAD and a 4Fe-4S cluster (By similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the ETF-QO / fixC family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U00048; AAB53835.2; -.
DR   WormBase; WBGene00002855; C05D11.12.
DR   WormPep; C05D11.12; CE29662.
DR   InterPro; IPR007859; ETFD.
DR   InterPro; IPR001100; Pyr_redox.
DR   Pfam; PF05187; ETF_QO; 1.
```

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DR   PRINTS; PR00411; PNDRDTASEI.
KW   4Fe-4S; Electron transport; FAD; Flavoprotein; Iron-sulfur;
KW   Mitochondrion; Oxidoreductase; Transit peptide; Transmembrane;
KW   Ubiquinone.
FT   TRANSIT       1      ?       Mitochondrion (Potential).
FT   CHAIN         ?    597       Probable electron transfer flavoprotein-
FT                                ubiquinone oxidoreductase.
FT   NP_BIND      53     67       FAD (ADP part) (Potential).
FT   TRANSMEM    437    457       Potential.
FT   METAL       540    540       Iron-sulfur (4Fe-4S) (Potential).
FT   METAL       566    566       Iron-sulfur (4Fe-4S) (Potential).
FT   METAL       569    569       Iron-sulfur (4Fe-4S) (Potential).
FT   METAL       572    572       Iron-sulfur (4Fe-4S) (Potential).
SQ   SEQUENCE   597 AA;  65335 MW;  C0FF09F185A017FB CRC64;

  Query Match             66.1%;  Score 37;  DB 1;  Length 597;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              ||| ||:|
Db        283 QYGGSFLY 290


Search completed: September 11, 2005, 02:55:42
Job time : 127.556 secs
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:44:10 ; Search time 26.1111 Seconds
(without alignments)
36.849 Million cell updates/sec

Title: US-10-684-957-44
Perfect score: 56
Sequence: 1 QQYGNSFMYT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	69.6	293	2	F98354	algM2 (AB011415) [
2	39	69.6	293	2	AI2927	hypothetical prote
3	38	67.9	340	2	E90975	probable integrase
4	38	67.9	340	2	C85822	probable integrase
5	37	66.1	260	2	T15237	hypothetical prote
6	37	66.1	618	2	D88483	protein let-721 [i
7	37	66.1	1431	2	T22748	hypothetical prote
8	37	66.1	1564	2	T27121	hypothetical prote
9	36	64.3	91	2	S25462	Ig kappa chain V r
10	36	64.3	93	2	S37528	Ig kappa chain V r
11	36	64.3	104	2	PH0964	Ig kappa chain V r
12	36	64.3	107	2	S26343	Ig kappa chain V r
13	36	64.3	107	2	S26344	Ig kappa chain V r
14	36	64.3	111	1	KVMS37	Ig kappa chain V r
15	36	64.3	131	1	KVMSM6	Ig kappa chain pre
16	36	64.3	276	2	AD1210	DTDP-L-rhamnose sy
17	36	64.3	283	2	B69769	hypothetical prote
18	36	64.3	304	2	H75081	phosphate abc tran
19	36	64.3	317	1	C71239	hypothetical prote
20	36	64.3	414	2	F96553	unknown protein, 3
21	36	64.3	558	2	S38614	hypothetical prote
22	36	64.3	852	2	T01364	homeodomain transc
23	35.5	63.4	450	2	G83740	hypothetical prote
24	35	62.5	93	2	S37505	Ig kappa chain V r
25	35	62.5	589	2	AD2263	hypothetical prote
26	35	62.5	720	2	A44819	alpha-galactosidas
27	35	62.5	720	2	H95221	alpha-galactosidas
28	35	62.5	720	2	G98085	alpha-galactosidas
29	34	60.7	93	2	S37501	Ig kappa chain V r
30	34	60.7	114	2	S46375	Ig kappa chain V-J
31	34	60.7	129	2	S40325	Ig kappa chain - h
32	34	60.7	132	1	KVMS32	Ig kappa chain pre
33	34	60.7	464	2	D90281	hypothetical prote
34	34	60.7	465	2	E69788	hypothetical prote
35	34	60.7	509	2	E89787	hypothetical prote
36	34	60.7	517	2	T02192	probable cytochrom
37	34	60.7	526	2	T02191	cytochrome P450 ho
38	34	60.7	563	2	A75594	ferredoxin-nitrite
39	34	60.7	599	2	I53395	antigen LEC-A - mo
40	34	60.7	685	2	T09159	RNA helicase prh75
41	34	60.7	713	2	A35502	major surface-labe
42	34	60.7	745	2	T23893	hypothetical prote
43	34	60.7	1026	2	S51432	hypothetical prote
44	33	58.9	99	2	JH0429	Ig kappa chain V-I
45	33	58.9	100	1	K3HUNG	Ig kappa chain pre

ALIGNMENTS

RESULT 1
F98354
algM2 (AB011415) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F98354
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F98354
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-293 <KUR>
A;Cross-references: UNIPROT:Q8UBJ3; GB:AE007870; PIDN:AAK90360.1; PID:g15160402; GSPDB:
C;Genetics:
A;Gene: AGR_L_3561
A;Map position: linear chromosome
C;Superfamily: maltose transport protein malG

Query Match 69.6%; Score 39; DB 2; Length 293;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 YGNSFMYT 10
              |||:|:||
Db         77 YGNTFIYT 84
```

RESULT 2
AI2927
hypothetical protein Atu3023 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI2927
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2927
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-293 <KUR>
A;Cross-references: UNIPROT:Q8UBJ3; GB:AE008689; PIDN:AAL43839.1; PID:g17741381; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3023

```
A;Map position: linear chromosome
C;Superfamily: maltose transport protein malG

  Query Match           69.6%;  Score 39;  DB 2;  Length 293;
  Best Local Similarity  75.0%;  Pred. No. 6.5;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMYT 10
              |||:|:||
Db         77 YGNTFIYT 84


RESULT 3
E90975
probable integrase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E90975
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90975
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <HAY>
A;Cross-references: UNIPROT:Q8X8W9; GB:BA000007; PIDN:BAB36196.1; PID:g13362241; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2773

  Query Match           67.9%;  Score 38;  DB 2;  Length 340;
  Best Local Similarity  75.0%;  Pred. No. 12;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db        250 QYGNRYMY 257


RESULT 4
C85822
probable integrase for prophage CP-933U intU [imported] - Escherichia coli (strain O157:
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85822
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85822
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <STO>
A;Cross-references: UNIPROT:Q8X8W9; GB:AE005174; NID:g12516149; PIDN:AAG57039.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: intU

  Query Match           67.9%;  Score 38;  DB 2;  Length 340;
  Best Local Similarity  75.0%;  Pred. No. 12;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              |||| :||
Db        250 QYGNRYMY 257


RESULT 5
T15237
hypothetical protein F56F4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15237
R;Murray, J.; Wohldmann, P.; Gillam, B.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F56F4.
A;Reference number: Z18313
A;Accession: T15237
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <MUR>
A;Cross-references: UNIPROT:O01842; EMBL:AF003146; NID:g2088769; PID:g2088775; PIDN:AAB5
A;Experimental source: strain Bristol N2; clone F56F4
C;Genetics:
A;Gene: CESP:F56F4.6
A;Map position: 1
A;Introns: 56/3; 75/2

  Query Match           66.1%;  Score 37;  DB 2;  Length 260;
  Best Local Similarity  66.7%;  Pred. No. 14;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMYT 10
              ||||::| |
Db        164 QYGNTYMMT 172


RESULT 6
D88483
protein let-721 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: D88483
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: D88483
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-618 <STO>
A;Cross-references: GB:chr_III; PIDN:AAB53835.1; PID:g1216303; GSPDB:GN00021; CESP:let-7
C;Genetics:
A;Gene: let-721
A;Map position: 3

  Query Match           66.1%;  Score 37;  DB 2;  Length 618;
  Best Local Similarity  75.0%;  Pred. No. 35;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMY 9
              ||| ||:|
Db        304 QYGGSFLY 311


RESULT 7
T22748
hypothetical protein F55G11.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T22748
R;Baynes, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19608
A;Accession: T22748
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1431 <WIL>
A;Cross-references: UNIPROT:Q9XUD4; EMBL:Z82272; PIDN:CAB05222.1; GSPDB:GN00022; CESP:F5
A;Experimental source: clone F55G11
C;Genetics:
```

```
A;Gene: CESP:F55G11.9
A;Map position: 4
A;Introns: 43/3; 86/2; 141/2; 225/3; 351/1; 704/3; 810/1; 836/1; 847/1; 906/3; 950/2; 10
C;Superfamily: ATP-binding cassette homology

  Query Match             66.1%;  Score 37;  DB 2;  Length 1431;
  Best Local Similarity   66.7%;  Pred. No. 84;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMYT 10
              ||||::| |
Db       1343 QYGNTYMMT 1351


RESULT 8
T27121
hypothetical protein Y53C10A.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T27121
R;White, S.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z20314
A;Accession: T27121
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1564 <WIL>
A;Cross-references: UNIPROT:Q9XW49; EMBL:AL033536; PIDN:CAA22142.1; CESP:Y53C10A.9
A;Experimental source: clone Y53C10A
C;Genetics:
A;Gene: CESP:Y53C10A.9
A;Introns: 43/3; 92/2; 148/2; 226/3; 354/1; 712/3; 817/1; 875/1; 916/3; 984/3; 1069/2; 1
C;Superfamily: ATP-binding cassette homology

  Query Match             66.1%;  Score 37;  DB 2;  Length 1564;
  Best Local Similarity   66.7%;  Pred. No. 92;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYGNSFMYT 10
              ||||::| |
Db       1464 QYGNTYMMT 1472


RESULT 9
S25462
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25462
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core histone
A;Reference number: S25174
A;Accession: S25462
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <MON>
A;Cross-references: EMBL:X67623; NID:g52188; PIDN:CAA47881.1; PID:g938263
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             64.3%;  Score 36;  DB 2;  Length 91;
  Best Local Similarity   85.7%;  Pred. No. 7.2;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 10
S37528
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37528
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral bloo
A;Reference number: S37501
A;Accession: S37528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <KLE>
A;Cross-references: EMBL:Z26616; NID:g405698; PIDN:CAA81369.1; PID:g405699
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             64.3%;  Score 36;  DB 2;  Length 93;
  Best Local Similarity   70.0%;  Pred. No. 7.4;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||:|  ||
Db         73 QQYGSSPQYT 82


RESULT 11
PH0964
Ig kappa chain V region (G6+ CLL-SIC) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PH0964
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0964
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-104 <MAR>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-21/Region: framework 1
F;14-89/Domain: immunoglobulin homology <IMM>
F;22-32/Region: complementarity-determining 1
F;33-48/Region: framework 2
F;49-54/Region: complementarity-determining 2
F;55-87/Region: framework 3
F;88-92/Region: complementarity-determining 3

  Query Match             64.3%;  Score 36;  DB 2;  Length 104;
  Best Local Similarity   85.7%;  Pred. No. 8.3;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYGNSF 7
              |||||:|
Db         88 QQYGNTF 94


RESULT 12
S26343
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26343
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26343
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107.<STA>
A;Cross-references: EMBL:X59207; NID:g52334; PIDN:CAA41917.1; PID:g1334073
```

```
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

  Query Match             64.3%;  Score 36;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 8.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         31 YGNSFMH 37


RESULT 13
S26344
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26344
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PID:g1334074
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

  Query Match             64.3%;  Score 36;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 8.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         31 YGNSFMH 37


RESULT 14
KVMS37
Ig kappa chain V regions (PC3741, T111) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A93204; A93822; A01934
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC3741
A;Accession: A93204
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01660
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: T111
A;Accession: A93822
A;Molecule type: protein
A;Residues: 1-111 <MCK>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

  Query Match             64.3%;  Score 36;  DB 1;  Length 111;
  Best Local Similarity   85.7%;  Pred. No. 8.9;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGNSFMY 9
              ||||||:
Db         32 YGNSFMH 38


RESULT 15
KVMSM6
Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: B90412; B90374; B93822; C93822; C93204; D93204; PH1078; A01935
R;Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A;Title: Primary structures of N-terminal extra peptide segments linked to the variable
expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: M63
A;Accession: B90412
A;Molecule type: protein
A;Residues: 1-35 <BUR>
A;Cross-references: UNIPROT:P01661
R;McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A;Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains
A;Reference number: A90374; MUID:73140225; PMID:4691517
A;Contents: M63
A;Accession: B90374
A;Molecule type: protein
A;Residues: 21-46,'Q',48-53,'B',55-57,'Z',59-86,'F',88-131 <MCK>
A;Note: this sequence has since been revised in reference A93822
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: M63; AB22
A;Accession: B93822
A;Molecule type: protein
A;Residues: 1-53;69-107 <MC2>
A;Accession: C93822
A;Molecule type: protein
A;Residues: 21-119,'Y',121-131 <MC3>
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC9245; PC4050
A;Accession: C93204
A;Molecule type: protein
A;Residues: 21-119,'Y',121-131 <WEI>
A;Accession: D93204
A;Molecule type: protein
A;Residues: 21-119,'L',121-123,'A',125-129,'L',131 <WE2>
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1078
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 21-122 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
C;Comment: The M63 precursor sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>
F;43-112/Disulfide bonds: #status predicted
```

Query Match 64.3%; Score 36; DB 1; Length 131;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 YGNSFMY 9
              ||||||:
Db         52 YGNSFMH 58
```

Search completed: September 11, 2005, 02:56:33
Job time : 27.1111 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:40:25 ; Search time 131.667 Seconds
(without alignments)
29.374 Million cell updates/sec

Title: US-10-684-957-44
Perfect score: 56
Sequence: 1 QQYGNSFMYT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	56	100.0	10	8	ADS87951	Ads87951 Anti-IFN-
2	56	100.0	10	8	ADS94948	Ads94948 Anti-IFN-
3	56	100.0	109	8	ADS87938	Ads87938 Anti-IFN-
4	56	100.0	109	8	ADS94935	Ads94935 Anti-IFN-
5	56	100.0	216	8	ADS87940	Ads87940 Anti-IFN-
6	56	100.0	216	8	ADS94937	Ads94937 Anti-IFN-
7	41	73.2	226	4	AAB99394	Aab99394 Human int
8	41	73.2	226	4	AAB75027	Aab75027 Anti-IL8
9	40	71.4	103	2	AAR47933	Aar47933 Light cha
10	40	71.4	103	2	AAW89349	Aaw89349 Mouse 23F
11	40	71.4	111	2	AAR47935	Aar47935 Humanised
12	40	71.4	111	2	AAW89351	Aaw89351 Humanised
13	39	69.6	10	6	AAE38105	Aae38105 Human COU
14	39	69.6	104	6	AAE38115	Aae38115 Human can
15	38	67.9	131	6	ABP57366	Abp57366 Anti-TRAI
16	38	67.9	340	7	ADC00770	Adc00770 Enterohae
17	38	67.9	500	2	AAR27742	Aar27742 Sequence
18	38	67.9	870	2	AAW19725	Aaw19725 Truncated
19	38	67.9	2410	2	AAW19723	Aaw19723 Cell cycl
20	38	67.9	2480	2	AAW19724	Aaw19724 Cell cycl
21	38	67.9	2644	2	AAW13152	Aaw13152 Human ata
22	38	67.9	2644	2	AAW84271	Aaw84271 A human A
23	38	67.9	2644	6	ABP97120	Abp97120 Human ATR
24	38	67.9	2644	6	AAO30064	Aao30064 Human ATR
25	38	67.9	2644	7	ADJ68378	Adj68378 Human hea
26	38	67.9	3029	8	ADP25433	Adp25433 Plasmodiu
27	37	66.1	134	2	AAW11155	Aaw11155 Anti-lung
28	37	66.1	260	8	ADN22410	Adn22410 Bacterial
29	37	66.1	1431	8	ADN23555	Adn23555 Bacterial
30	36	64.3	15	2	AAW27344	Aaw27344 CDR1 from
31	36	64.3	15	4	AAU07460	Aau07460 Synthetic
32	36	64.3	15	5	AAU70352	Aau70352 Mouse Kap
33	36	64.3	60	6	ABU56875	Abu56875 BoNT/A Hc
34	36	64.3	60	6	ABU56876	Abu56876 BoNT/A Hc
35	36	64.3	60	6	ABU56840	Abu56840 BoNT/A Hc
36	36	64.3	60	6	ABU56887	Abu56887 BoNT/A Hc
37	36	64.3	60	6	ABU56879	Abu56879 BoNT/A Hc
38	36	64.3	87	2	AAR80081	Aar80081 Mouse der
39	36	64.3	91	2	AAW95478	Aaw95478 Mouse der
40	36	64.3	107	2	AAW27353	Aaw27353 Light cha
41	36	64.3	111	2	AAR47494	Aar47494 Murine an
42	36	64.3	111	2	AAR47492	Aar47492 Humanised
43	36	64.3	111	2	AAR48622	Aar48622 Sequence
44	36	64.3	111	2	AAR48623	Aar48623 Sequence
45	36	64.3	111	2	AAR65172	Aar65172 Murine NM

ALIGNMENTS

RESULT 1
ADS87951
ID ADS87951 standard; peptide; 10 AA.
XX
AC ADS87951;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain CDR3 SEQ ID NO:44.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 2; SEQ ID NO 44; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36

CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 1 QQYGNSFMYT 10

RESULT 2
ADS94948
ID ADS94948 standard; peptide; 10 AA.
XX
AC ADS94948;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain CDR3 SEQ ID NO:44.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 2; SEQ ID NO 44; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 1 QQYGNSFMYT 10

RESULT 3
ADS87938
ID ADS87938 standard; protein; 109 AA.
XX
AC ADS87938;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:31.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87964.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX

PS Claim 9; SEQ ID NO 31; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 56; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 90 QQYGNSFMYT 99

RESULT 4
ADS94935
ID ADS94935 standard; protein; 109 AA.
XX
AC ADS94935;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:31.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94961.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 11; SEQ ID NO 31; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 56; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 90 QQYGNSFMYT 99

RESULT 5
ADS87940
ID ADS87940 standard; protein; 216 AA.
XX
AC ADS87940;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121* light chain SEQ ID NO:33.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.

XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 33; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 56; DB 8; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 90 QQYGNSFMYT 99

RESULT 6
ADS94937
ID ADS94937 standard; protein; 216 AA.
XX
AC ADS94937;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121* light chain SEQ ID NO:33.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 33; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 56; DB 8; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||||||||
Db 90 QQYGNSFMYT 99

RESULT 7
AAB99394
ID AAB99394 standard; protein; 226 AA.
XX
AC AAB99394;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody protein sequence M2_20L.
XX
KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200140306-A1.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US033042.
XX
PR 06-DEC-1999; 99US-00456090.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;

XX
DR WPI; 2001-374798/39.
XX
PT Detecting analyte in human sample containing human antibodies binding to
PT nonhuman-antibodies, involves contacting sample with human antibody which
PT binds to antibodies from nonhuman species and detecting binding.
XX
PS Example 22; Page 96; 135pp; English.
XX
CC The present invention describes a method for detecting an analyte in a
CC human sample containing human antibodies that specifically bind to
CC antibodies from a nonhuman species. The method involves contacting the
CC sample with a human antibody (I) which specifically binds to antibodies
CC from a nonhuman species and detecting the binding between (I) and the
CC analyte to indicate presence of the analyte. The method is used for
CC detecting an analyte in a human sample containing human anti-mouse
CC antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC heterophilic antibodies). The method can also be used for detecting any
CC type of target antigen including bacterial, fungal and viral pathogens
CC that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC aeruginosa. Human antibodies can be used as detection reagents for
CC performing clinical diagnostic tests and for performing other in vitro
CC detection assays, including for research purposes. (I) can be used in
CC qualitative assays designed to indicate the presence of one or more
CC target antigens above minimally detectable amounts of antigen in the
CC sample that usually correspond to the sensitivity limitations of the
CC assays for each target antigen. Also, (I) is used to determine the amount
CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 226 AA;

Query Match 73.2%; Score 41; DB 4; Length 226;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||:| |||
Db 90 QQYGSSPMYT 99

RESULT 8
AAB75027
ID AAB75027 standard; protein; 226 AA.
XX
AC AAB75027;
XX
DT 19-JUL-2001 (first entry)
XX
DE Anti-IL8 monoclonal antibody protein fragment M2_20L.
XX
KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200125492-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-US027237.
XX
PR 02-OCT-1999; 99US-0157415P.
PR 01-DEC-1999; 99US-00453234.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR WPI; 2001-335567/35.
XX
PT Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS Example 22; Page 99-100; 161pp; English.
XX
CC The present invention describes a method (M1) for producing a human
CC antibody phage display library (I), comprising: (1) providing a nonhuman
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC (2) isolating nucleic acids encoding human antibody chains (III) from
CC lymphatic cells; and (3) forming a library of display packages whose
CC members comprise a nucleic acid encoding (III) which is displayed from
CC the package. The method is used for producing a human antibody display
CC library, e.g., a Fab phage display library. The display method may be
CC used to screen nucleic acids encoding antibody chains obtained from
CC immunised nonhuman transgenic animals, and from this a population of
CC antibodies may be prepared. Production of a human monoclonal antibodies
CC display library using this method means there is no need to immunise
CC humans with antigens, and the difficulties faced with immortalising B
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 226 AA;

Query Match 73.2%; Score 41; DB 4; Length 226;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||:| |||
Db 90 QQYGSSPMYT 99

RESULT 9
AAR47933
ID AAR47933 standard; protein; 103 AA.
XX
AC AAR47933;
XX
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 24-JUL-1994 (first entry)
XX
DE Light chain region of 23F2G.
XX
KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;
KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;
KW monoclonal antibody; LFA-1; adhesion; migration; multiple sclerosis; MS.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO9402175-A1.
XX
PD 03-FEB-1994.
XX
PF 16-JUL-1993; 93WO-US006734.
XX
PR 16-JUL-1992; 92US-00915068.
PR 10-MAY-1993; 93US-00060699.
XX
PA (ICOS-) ICOS CORP.
PA (UNIW) UNIV WASHINGTON.
XX
PI Rose LM;
XX
DR WPI; 1994-048551/06.
DR N-PSDB; AAQ55915.
XX
PT Antibodies immunologically reactive with the CD18 of human leukocyte

```
PT   integrins and/or competing with mAb 60.3 for binding to human LFA-1 - for
PT   alleviating symptoms associated with inflammatory disease states.
XX
PS   Example 6; Page 43; 58pp; English.
XX
CC   Total RNA was isolated from the hybridoma cell line 23F2G and first
CC   strand cDNA was synthesised using the total RNA as a template. The first
CC   strand cDNA was used as a template for PCR to obtain double stranded DNA
CC   fragments encoding the variable regions of both the heavy and light
CC   chains of monoclonal antibody 23F2G. The sequence shown is that of the
CC   light chain variable region of MAb 23F2G The humanised form of MAb 23F2G
CC   may be administered to alleviate symptoms associated with inflammatory
CC   disease states, esp. for the inhibition of inflammatory processes
CC   associated with multiple sclerosis. The MAb blocks leukocyte adhesion and
CC   migration to inflammatory sites. The MAb is an anti-CD18 integrin
CC   antibody which competes with MAb 60.3 for binding to LFA-1. See also
CC   AAR47931-6. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 103 AA;

  Query Match             71.4%;  Score 40;  DB 2;  Length 103;
  Best Local Similarity   66.7%;  Pred. No. 23;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              : |||:|||
Db         22 ESYGNNFMY 30


RESULT 10
AAW89349
ID   AAW89349 standard; protein; 103 AA.
XX
AC   AAW89349;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Mouse 23F2G light chain variable region.
XX
KW   Mouse; humanised; antibody; heavy chain variable region; light chain;
KW   23F2G; inflammatory disease; multiple sclerosis; common beta chain; CD18;
KW   human leukocyte integrin.
XX
OS   Mus sp.
XX
PN   US5854070-A.
XX
PD   29-DEC-1998.
XX
PF   21-JAN-1997;   97US-00785571.
XX
PR   16-JUL-1992;   92US-00915068.
PR   10-MAY-1993;   93US-00060699.
PR   16-JUL-1993;   93US-00094535.
PR   28-FEB-1995;   95US-00396089.
XX
PA   (ICOS-) ICOS CORP.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Rose LM;
XX
DR   WPI; 1999-094920/08.
DR   N-PSDB; AAV81907.
XX
PT   Hybridomas that secrete anti-CD18 antibody - useful for treating
PT   inflammation specifically multiple sclerosis.
XX
PS   Example 6; Col 25-26; 24pp; English.
XX
CC   The present invention describes the hybridoma cell line 23F2G (ATCC HB
CC   11801) and the Chinese hamster ovary (CHO) cell lines 6E6 (ATCC CRL
CC   11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (MAb) 23F2G (and
CC   its humanised variants 6E6 and B13-24) is an anti-human CD18 antibody for
CC   the treatment of inflammation, specifically multiple sclerosis. The
CC   present sequence is mouse 23F2G light chain variable region from the
CC   present invention
XX
SQ   Sequence 103 AA;

  Query Match             71.4%;  Score 40;  DB 2;  Length 103;
  Best Local Similarity   66.7%;  Pred. No. 23;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              : |||:|||
Db         22 ESYGNNFMY 30


RESULT 11
AAR47935
ID   AAR47935 standard; protein; 111 AA.
XX
AC   AAR47935;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   24-JUL-1994  (first entry)
XX
DE   Humanised light chain region of 23F2G.
XX
KW   Amplification; 23F2G; humanised antibody; heavy chain; light chain;
KW   hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;
KW   monoclonal antibody; LFA-1; adhesion; migration; multiple sclerosis; MS.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9402175-A1.
XX
PD   03-FEB-1994.
XX
PF   16-JUL-1993;   93WO-US006734.
XX
PR   16-JUL-1992;   92US-00915068.
PR   10-MAY-1993;   93US-00060699.
XX
PA   (ICOS-) ICOS CORP.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Rose LM;
XX
DR   WPI; 1994-048551/06.
DR   N-PSDB; AAQ55917.
XX
PT   Antibodies immunologically reactive with the CD18 of human leukocyte
PT   integrins and/or competing with mAb 60.3 for binding to human LFA-1 - for
PT   alleviating symptoms associated with inflammatory disease states.
XX
PS   Example 6; Page 45; 58pp; English.
XX
CC   Total RNA was isolated from the hybridoma cell line 23F2G and first
CC   strand cDNA was synthesised using the total RNA as a template. The first
CC   strand cDNA was used as a template for PCR to obtain double stranded DNA
CC   fragments encoding the variable regions of both the heavy and light
CC   chains of monoclonal antibody 23F2G. The sequence shown is a humanised
CC   form of the light chain variable region of MAb 23F2G. The humanised form
CC   of MAb 23F2G may be administered to alleviate symptoms associated with
CC   inflammatory disease states, esp. for the inhibition of inflammatory
CC   processes associated with multiple sclerosis. The MAb blocks leukocyte
CC   adhesion and migration to inflammatory sites. The MAb is an anti-CD18
CC   integrin antibody which competes with MAb 60.3 for binding to LFA-1. See
CC   also AAR47931-6. (Updated on 10-MAR-2003 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 111 AA;
```

```
  Query Match             71.4%;  Score 40;  DB 2;  Length 111;
  Best Local Similarity   66.7%;  Pred. No. 24;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              : |||:|||
Db         30 ESYGNNFMY 38


RESULT 12
AAW89351
ID   AAW89351 standard; protein; 111 AA.
XX
AC   AAW89351;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Humanised 23F2G light chain variable region.
XX
KW   Mouse; humanised; antibody; heavy chain variable region; light chain;
KW   23F2G; inflammatory disease; multiple sclerosis; common beta chain; CD18;
KW   human leukocyte integrin.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US5854070-A.
XX
PD   29-DEC-1998.
XX
PF   21-JAN-1997;   97US-00785571.
XX
PR   16-JUL-1992;   92US-00915068.
PR   10-MAY-1993;   93US-00060699.
PR   16-JUL-1993;   93US-00094535.
PR   28-FEB-1995;   95US-00396089.
XX
PA   (ICOS-) ICOS CORP.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Rose LM;
XX
DR   WPI; 1999-094920/08.
DR   N-PSDB; AAV81909.
XX
PT   Hybridomas that secrete anti-CD18 antibody - useful for treating
PT   inflammation specifically multiple sclerosis.
XX
PS   Example 6; Col 27-30; 24pp; English.
XX
CC   The present invention describes the hybridoma cell line 23F2G (ATCC HB
CC   11801) and the Chinese hamster ovary (CHO) cell lines 6E6 (ATCC CRL
CC   11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (MAb) 23F2G (and
CC   its humanised variants 6E6 and B13-24) is an anti-human CD18 antibody for
CC   the treatment of inflammation, specifically multiple sclerosis. The
CC   present sequence represents humanised 23F2G light chain variable region
CC   from the present invention
XX
SQ   Sequence 111 AA;

  Query Match             71.4%;  Score 40;  DB 2;  Length 111;
  Best Local Similarity   66.7%;  Pred. No. 24;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMY 9
              : |||:|||
Db         30 ESYGNNFMY 38


RESULT 13
AAE38105
ID   AAE38105 standard; peptide; 10 AA.
XX
AC   AAE38105;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human COU-1 antibody VL CDR3 peptide #2.
XX
KW   Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
KW   adenocarcinoma; therapy; cancer; antibody; light chain variable region;
KW   complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO2003057168-A2.
XX
PD   17-JUL-2003.
XX
PF   03-JAN-2003; 2003WO-US000297.
XX
PR   03-JAN-2002; 2002US-0345208P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Ditzel H,  Jensenius JC;
XX
DR   WPI; 2003-598315/56.
XX
PT   Novel isolated cancer-associated epitope comprising two separate
PT   polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
PT   polypeptide, useful as component of vaccine for preventing or treating
PT   adenocarcinoma.
XX
PS   Claim 15; Page 36; 155pp; English.
XX
CC   The invention provides a cancer-associated epitope comprising two
CC   separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
CC   polypeptide. Vaccine composition of the invention is useful for treating
CC   or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
CC   adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
CC   adenocarcinoma or non-seminomal testis carcinoma. The invention is also
CC   useful for preparing a medicament for treating or preventing cancer in a
CC   mammal. The present sequence is human COU-1 cancer-associated epitope
CC   antibody VL (light chain variable region) CDR (complementarity
CC   determining region) peptide
XX
SQ   Sequence 10 AA;

  Query Match             69.6%;  Score 39;  DB 6;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 3.5;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYGNSFMYT 10
              ||||||  ||
Db          1 QQYGNSPPYT 10


RESULT 14
AAE38115
ID   AAE38115 standard; protein; 104 AA.
XX
AC   AAE38115;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human cancer-associated epitope antibody VL protein #1.
XX
KW   Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
KW   adenocarcinoma; therapy; cancer; antibody; light chain variable region.
XX
OS   Homo sapiens.
XX
PN   WO2003057168-A2.
```

XX
PD 17-JUL-2003.
XX
PF 03-JAN-2003; 2003WO-US000297.
XX
PR 03-JAN-2002; 2002US-0345208P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ditzel H, Jensenius JC;
XX
DR WPI; 2003-598315/56.
XX
PT Novel isolated cancer-associated epitope comprising two separate
PT polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
PT polypeptide, useful as component of vaccine for preventing or treating
PT adenocarcinoma.
XX
PS Claim 15; Page 41; 155pp; English.
XX
CC The invention provides a cancer-associated epitope comprising two
CC separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
CC polypeptide. Vaccine composition of the invention is useful for treating
CC or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
CC adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
CC adenocarcinoma or non-seminomal testis carcinoma. The invention is also
CC useful for preparing a medicament for treating or preventing cancer in a
CC mammal. The present sequence is human cancer-associated epitope antibody
CC VL (light chain variable region) protein
XX
SQ Sequence 104 AA;

Query Match 69.6%; Score 39; DB 6; Length 104;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||| ||
Db 86 QQYGNSPPYT 95

RESULT 15
ABP57366
ID ABP57366 standard; protein; 131 AA.
XX
AC ABP57366;
XX
DT 22-APR-2003 (first entry)
XX
DE Anti-TRAIL-R antibody related clone H-48-2 protein SEQ ID NO:27.
XX
KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
KW antibody therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200294880-A1.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-JP004816.
XX
PR 18-MAY-2001; 2001JP-00150213.
PR 09-AUG-2001; 2001JP-00243040.
PR 11-OCT-2001; 2001JP-00314489.
XX
PA (KIRI) KIRIN BEER KK.
XX
PI Mori E, Kataoka S;
XX
DR WPI; 2003-120790/11.
DR N-PSDB; ABZ59697.
XX
PT New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
PT nor inducing injury to hepatocytes, for use in therapy of malignant
PT tumor.
XX
PS Claim 54; Page 59; 92pp; Japanese.
XX
CC The present invention describes antibodies or their functional fragments
CC that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
CC have cytostatic and apoptotic activities, and can be used in antibody
CC therapy. The antibodies can be applied as remedies and preventives of
CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
CC in the therapy of malignant tumours. Remedies produced with the
CC antibodies are highly safe, and avoid hepatotoxicity. The present
CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
CC present invention
XX
SQ Sequence 131 AA;

Query Match 67.9%; Score 38; DB 6; Length 131;
Best Local Similarity 70.0%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYGNSFMYT 10
||||:| :||
Db 110 QQYGSSPLYT 119

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Job time : 132.667 secs

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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:55:51 ; Search time 97.7778 Seconds
(without alignments)
32.272 Million cell updates/sec

Title: US-10-684-957-37
Perfect score: 51
Sequence: 1 GSYWYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	100.0	117	17	US-10-684-957-10	Sequence 10, Appl
3	51	100.0	117	17	US-10-684-957-14	Sequence 14, Appl
4	51	100.0	117	17	US-10-684-957-30	Sequence 30, Appl
5	51	100.0	447	17	US-10-684-957-19	Sequence 19, Appl
6	51	100.0	447	17	US-10-684-957-21	Sequence 21, Appl
7	51	100.0	447	17	US-10-684-957-32	Sequence 32, Appl
8	45	88.2	10	17	US-10-842-011-17	Sequence 17, Appl
9	45	88.2	10	17	US-10-842-011-32	Sequence 32, Appl
10	45	88.2	15	13	US-10-153-159-47	Sequence 47, Appl
11	45	88.2	15	14	US-10-153-176-47	Sequence 47, Appl
12	45	88.2	15	15	US-10-443-134A-47	Sequence 47, Appl
13	45	88.2	19	13	US-10-153-159-49	Sequence 49, Appl
14	45	88.2	19	13	US-10-153-159-50	Sequence 50, Appl
15	45	88.2	19	13	US-10-153-159-51	Sequence 51, Appl
16	45	88.2	19	13	US-10-153-159-54	Sequence 54, Appl
17	45	88.2	19	13	US-10-153-159-57	Sequence 57, Appl
18	45	88.2	19	13	US-10-153-159-58	Sequence 58, Appl
19	45	88.2	19	13	US-10-153-159-59	Sequence 59, Appl
20	45	88.2	19	14	US-10-153-176-49	Sequence 49, Appl
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26	45	88.2	19	14	US-10-153-176-59	Sequence 59, Appl
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28	45	88.2	19	15	US-10-443-134A-50	Sequence 50, Appl
29	45	88.2	19	15	US-10-443-134A-51	Sequence 51, Appl
30	45	88.2	19	15	US-10-443-134A-54	Sequence 54, Appl
31	45	88.2	19	15	US-10-443-134A-57	Sequence 57, Appl
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34	45	88.2	20	10	US-09-880-748-3149	Sequence 3149, Ap
35	45	88.2	20	15	US-10-293-418-3149	Sequence 3149, Ap
36	45	88.2	26	13	US-10-153-159-74	Sequence 74, Appl
37	45	88.2	26	13	US-10-153-159-76	Sequence 76, Appl
38	45	88.2	26	13	US-10-153-159-77	Sequence 77, Appl
39	45	88.2	26	13	US-10-153-159-86	Sequence 86, Appl
40	45	88.2	26	13	US-10-153-159-87	Sequence 87, Appl
41	45	88.2	26	13	US-10-153-159-91	Sequence 91, Appl
42	45	88.2	26	13	US-10-153-159-125	Sequence 125, App
43	45	88.2	26	14	US-10-153-176-74	Sequence 74, Appl
44	45	88.2	26	14	US-10-153-176-76	Sequence 76, Appl
45	45	88.2	26	14	US-10-153-176-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-10-684-957-37
; Sequence 37, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-ga
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-37

Query Match 100.0%; Score 51; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 1 GSYWYFDL 8

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RESULT 2
US-10-684-957-10
; Sequence 10, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-10

  Query Match             100.0%;  Score 51;  DB 17;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db         99 GSYWYFDL 106


RESULT 3
US-10-684-957-14
; Sequence 14, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-14

  Query Match             100.0%;  Score 51;  DB 17;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db         99 GSYWYFDL 106


RESULT 4
US-10-684-957-30
; Sequence 30, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-684-957-30

  Query Match             100.0%;  Score 51;  DB 17;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db         99 GSYWYFDL 106


RESULT 5
US-10-684-957-19
; Sequence 19, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-19

  Query Match             100.0%;  Score 51;  DB 17;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db         99 GSYWYFDL 106
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RESULT 6
US-10-684-957-21
; Sequence 21, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-21

  Query Match             100.0%;  Score 51;  DB 17;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db         99 GSYWYFDL 106


RESULT 7
US-10-684-957-32
; Sequence 32, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-32

  Query Match             100.0%;  Score 51;  DB 17;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db         99 GSYWYFDL 106


RESULT 8
US-10-842-011-17
; Sequence 17, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: 05882.0110.NPUS04
;  CURRENT APPLICATION NUMBER: US/10/842,011
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-842-011-17

  Query Match             88.2%;  Score 45;  DB 17;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 2.9;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |:|||||:
Db          3 GNYWYFDV 10


RESULT 9
US-10-842-011-32
; Sequence 32, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: 05882.0110.NPUS04
;  CURRENT APPLICATION NUMBER: US/10/842,011
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-842-011-32

  Query Match             88.2%;  Score 45;  DB 17;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 2.9;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |:|||||:
Db          3 GNYWYFDV 10


RESULT 10
US-10-153-159-47
; Sequence 47, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Peter
;  APPLICANT:  Hsieh, Mark
;  APPLICANT:  Zhong, Pingyu
;  APPLICANT:  Wang, Caili
;  TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LI
;  TITLE OF INVENTION:  SILICO
;  FILE REFERENCE: 26050-704
;  CURRENT APPLICATION NUMBER: US/10/153,159
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: US 10/125,687
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: US 60/284,407
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 47
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR3 Variant
US-10-153-159-47

Query Match 88.2%; Score 45; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SYWYFDL 8
|||||||
Db 9 SYWYFDL 15

RESULT 11
US-10-153-176-47
; Sequence 47, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR3 Variant
US-10-153-176-47

Query Match 88.2%; Score 45; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SYWYFDL 8
|||||||
Db 9 SYWYFDL 15

RESULT 12
US-10-443-134A-47
; Sequence 47, Application US/10443134A
; Publication No. US20040010376A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
; FILE REFERENCE: 26050-709
; CURRENT APPLICATION NUMBER: US/10/443,134A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/153,159
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR3 Variant
US-10-443-134A-47

Query Match 88.2%; Score 45; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SYWYFDL 8
|||||||
Db 9 SYWYFDL 15

RESULT 13
US-10-153-159-49
; Sequence 49, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
; TITLE OF INVENTION: SILICO
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant #61
US-10-153-159-49

Query Match 88.2%; Score 45; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SYWYFDL 8
|||||||
Db 11 SYWYFDL 17

RESULT 14
US-10-153-159-50
; Sequence 50, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
; TITLE OF INVENTION: SILICO

```
;  FILE REFERENCE: 26050-704
;  CURRENT APPLICATION NUMBER: US/10/153,159
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: US 10/125,687
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: US 60/284,407
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Variant #181
US-10-153-159-50

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  Best Local Similarity   100.0%;  Pred. No. 5;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              |||||||
Db         11 SYWYFDL 17


RESULT 15
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; Sequence 51, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Peter
;  APPLICANT:  Hsieh, Mark
;  APPLICANT:  Zhong, Pingyu
;  APPLICANT:  Wang, Caili
;  TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
;  TITLE OF INVENTION:  SILICO
;  FILE REFERENCE: 26050-704
;  CURRENT APPLICATION NUMBER: US/10/153,159
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: US 10/125,687
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: US 60/284,407
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Variant #19501
US-10-153-159-51

  Query Match             88.2%;  Score 45;  DB 13;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              |||||||
Db         11 SYWYFDL 17


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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:45:00 ; Search time 26.6667 Seconds
(without alignments)
22.395 Million cell updates/sec

Title: US-10-684-957-37
Perfect score: 51
Sequence: 1 GSYWYFDL 8

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	84.3	17	4	US-09-440-781-63	Sequence 63, Appl
2	43	84.3	17	4	US-09-440-781-64	Sequence 64, Appl
3	43	84.3	17	4	US-09-440-781-66	Sequence 66, Appl
4	42	82.4	10	2	US-08-480-434-28	Sequence 28, Appl
5	42	82.4	10	2	US-08-480-434-35	Sequence 35, Appl
6	42	82.4	10	2	US-08-053-451B-28	Sequence 28, Appl
7	42	82.4	10	2	US-08-053-451B-35	Sequence 35, Appl
8	42	82.4	119	2	US-08-053-451B-125	Sequence 125, App
9	42	82.4	121	2	US-08-480-434-29	Sequence 29, Appl
10	42	82.4	121	2	US-08-053-451B-29	Sequence 29, Appl
11	42	82.4	123	4	US-09-726-653-1	Sequence 1, Appli
12	42	82.4	123	4	US-09-726-653-2	Sequence 2, Appli
13	42	82.4	123	4	US-09-726-653-3	Sequence 3, Appli
14	42	82.4	123	4	US-09-726-653-7	Sequence 7, Appli
15	42	82.4	123	4	US-09-726-653-9	Sequence 9, Appli
16	42	82.4	123	4	US-09-726-653-10	Sequence 10, Appl
17	42	82.4	123	4	US-09-726-653-11	Sequence 11, Appl
18	42	82.4	123	4	US-09-726-653-12	Sequence 12, Appl
19	42	82.4	123	4	US-09-726-653-13	Sequence 13, Appl
20	42	82.4	123	4	US-09-726-653-14	Sequence 14, Appl
21	42	82.4	123	4	US-09-726-653-15	Sequence 15, Appl
22	42	82.4	124	4	US-09-726-653-18	Sequence 18, Appl
23	42	82.4	126	2	US-08-480-434-18	Sequence 18, Appl
24	42	82.4	126	2	US-08-480-434-19	Sequence 19, Appl
25	42	82.4	126	2	US-08-053-451B-18	Sequence 18, Appl
26	42	82.4	126	2	US-08-053-451B-19	Sequence 19, Appl
27	42	82.4	140	4	US-09-724-138-44	Sequence 44, Appl
28	41	80.4	380	4	US-09-248-796A-15708	Sequence 15708, A
29	41	80.4	502	4	US-09-134-000C-5273	Sequence 5273, Ap
30	39	76.5	11	2	US-08-452-724A-31	Sequence 31, Appl
31	39	76.5	11	4	US-08-453-623-31	Sequence 31, Appl
32	39	76.5	15	3	US-08-525-539A-38	Sequence 38, Appl
33	39	76.5	113	1	US-07-942-245-19	Sequence 19, Appl
34	39	76.5	121	1	US-08-077-252B-2	Sequence 2, Appli
35	39	76.5	121	3	US-09-002-753A-2	Sequence 2, Appli
36	39	76.5	121	4	US-09-657-274-2	Sequence 2, Appli
37	39	76.5	121	5	PCT-US94-06687-2	Sequence 2, Appli
38	39	76.5	122	1	US-08-107-669D-6	Sequence 6, Appli
39	39	76.5	122	1	US-08-472-788A-6	Sequence 6, Appli
40	39	76.5	122	2	US-08-477-531B-6	Sequence 6, Appli
41	39	76.5	122	2	US-08-082-842A-6	Sequence 6, Appli
42	39	76.5	122	4	US-09-232-290-56	Sequence 56, Appl
43	39	76.5	123	4	US-09-726-653-16	Sequence 16, Appl
44	39	76.5	277	2	US-08-256-790-2	Sequence 2, Appli
45	38	74.5	11	2	US-08-483-636-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-440-781-63
; Sequence 63, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yee Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 63
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-63

Query Match 84.3%; Score 43; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.74;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GSYWYFDL 8
              ||:||||:
Db         10 GSHWYFDV 17
```

RESULT 2
US-09-440-781-64
; Sequence 64, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yee Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 64
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-64

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  Query Match             84.3%;  Score 43;  DB 4;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 0.74;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||:||||:
Db         10 GSHWYFDV 17


RESULT 3
US-09-440-781-66
; Sequence 66, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
;  APPLICANT: Yvonne Man-yee Chen et al.
;  TITLE OF INVENTION: ANTIBODY VARIANTS
;  FILE REFERENCE: P1469R1
;  CURRENT APPLICATION NUMBER: US/09/440,781
;  CURRENT FILING DATE: 1999-11-16
;  NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 66
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: artificial
;   LOCATION: 1-17
;   OTHER INFORMATION: variant CDR sequence
US-09-440-781-66

  Query Match             84.3%;  Score 43;  DB 4;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 0.74;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||:||||:
Db         10 GSHWYFDV 17


RESULT 4
US-08-480-434-28
; Sequence 28, Application US/08480434
; Patent No. 5811248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles C. Ditlow, et al.
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;    TITLE OF INVENTION:  ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,434
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Albert P. Halluin
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-3660
;      TELEFAX:  (415) 854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-480-434-28

  Query Match             82.4%;  Score 42;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 0.63;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db          3 GYYWYFDV 10


RESULT 5
US-08-480-434-35
; Sequence 35, Application US/08480434
; Patent No. 5811248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles C. Ditlow, et al.
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;    TITLE OF INVENTION:  ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,434
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Albert P. Halluin
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-3660
;      TELEFAX:  (415) 854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-480-434-35

  Query Match             82.4%;  Score 42;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 0.63;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db          3 GYYWYFDV 10
```

```
RESULT 6
US-08-053-451B-28
; Sequence 28, Application US/08053451B
; Patent No. 5955584
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Francis W.
;    APPLICANT:  Ditlow, Charles C.
;    APPLICANT:  Calenoff, Emanuel
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC
;    TITLE OF INVENTION:  ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,451B
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-033-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-053-451B-28

  Query Match             82.4%;  Score 42;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 0.63;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db          3 GYYWYFDV 10


RESULT 7
US-08-053-451B-35
; Sequence 35, Application US/08053451B
; Patent No. 5955584
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Francis W.
;    APPLICANT:  Ditlow, Charles C.
;    APPLICANT:  Calenoff, Emanuel
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC
;    TITLE OF INVENTION:  ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,451B
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-033-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-053-451B-35

  Query Match             82.4%;  Score 42;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 0.63;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db          3 GYYWYFDV 10


RESULT 8
US-08-053-451B-125
; Sequence 125, Application US/08053451B
; Patent No. 5955584
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Francis W.
;    APPLICANT:  Ditlow, Charles C.
;    APPLICANT:  Calenoff, Emanuel
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC
;    TITLE OF INVENTION:  ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,451B
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-033-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  125:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-053-451B-125

  Query Match             82.4%;  Score 42;  DB 2;  Length 119;
  Best Local Similarity   75.0%;  Pred. No. 7.7;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db        101 GYYWYFDV 108


RESULT 9
US-08-480-434-29
; Sequence 29, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
;    APPLICANT:  Charles C. Ditlow, et al.
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;    TITLE OF INVENTION:  ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,434
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Albert P. Halluin
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-3660
;      TELEFAX:  (415) 854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  121 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-480-434-29

  Query Match             82.4%;  Score 42;  DB 2;  Length 121;
  Best Local Similarity   75.0%;  Pred. No. 7.8;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db        103 GYYWYFDV 110


RESULT 10
US-08-053-451B-29
; Sequence 29, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
;    APPLICANT:  Chen, Francis W.
;    APPLICANT:  Ditlow, Charles C.
;    APPLICANT:  Calenoff, Emanuel
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC
;    TITLE OF INVENTION:  ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,451B
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-033-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  121 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-053-451B-29

  Query Match             82.4%;  Score 42;  DB 2;  Length 121;
  Best Local Similarity   75.0%;  Pred. No. 7.8;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db        103 GYYWYFDV 110


RESULT 11
US-09-726-653-1
; Sequence 1, Application US/09726653
; Patent No. 6680192
; GENERAL INFORMATION:
;  APPLICANT: LERNER, Richard A.
;  APPLICANT:  WINTER, Gregory P.
;  APPLICANT:  RIECHMAN, Lutz
;  APPLICANT:  HUSE, William D.
;  APPLICANT:  SORGE, Joseph A.
;  TITLE OF INVENTION: A METHOD FOR PRODUCING POLYMERS HAVING A PRESELECTED ACTIVITY
;  FILE REFERENCE: 062710013DVUS01
;  CURRENT APPLICATION NUMBER: US/09/726,653
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 07/941,761
;  PRIOR FILING DATE: 1992-09-04
;  PRIOR APPLICATION NUMBER: 07/799,772
;  PRIOR FILING DATE: 1991-11-27
;  PRIOR APPLICATION NUMBER: 07/496,522
;  PRIOR FILING DATE: 1990-03-20
;  PRIOR APPLICATION NUMBER: 07/410,716
```

```
;  PRIOR FILING DATE: 1989-09-20
;  PRIOR APPLICATION NUMBER: 07/352,927
;  PRIOR FILING DATE: 1989-05-16
;  PRIOR APPLICATION NUMBER: 07/411,058
;  PRIOR FILING DATE: 1989-09-21
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(123)
;   OTHER INFORMATION: HPCM2-hybridoma
US-09-726-653-1

  Query Match             82.4%;  Score 42;  DB 4;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 7.9;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 12
US-09-726-653-2
; Sequence 2, Application US/09726653
; Patent No. 6680192
; GENERAL INFORMATION:
;  APPLICANT: LERNER, Richard A.
;  APPLICANT:  WINTER, Gregory P.
;  APPLICANT:  RIECHMAN, Lutz
;  APPLICANT:  HUSE, William D.
;  APPLICANT:  SORGE, Joseph A.
;  TITLE OF INVENTION: A METHOD FOR PRODUCING POLYMERS HAVING A PRESELECTED ACTIVITY
;  FILE REFERENCE: 062710013DVUS01
;  CURRENT APPLICATION NUMBER: US/09/726,653
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 07/941,761
;  PRIOR FILING DATE: 1992-09-04
;  PRIOR APPLICATION NUMBER: 07/799,772
;  PRIOR FILING DATE: 1991-11-27
;  PRIOR APPLICATION NUMBER: 07/496,522
;  PRIOR FILING DATE: 1990-03-20
;  PRIOR APPLICATION NUMBER: 07/410,716
;  PRIOR FILING DATE: 1989-09-20
;  PRIOR APPLICATION NUMBER: 07/352,927
;  PRIOR FILING DATE: 1989-05-16
;  PRIOR APPLICATION NUMBER: 07/411,058
;  PRIOR FILING DATE: 1989-09-21
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(123)
;   OTHER INFORMATION: HPCM3-hybridoma
US-09-726-653-2

  Query Match             82.4%;  Score 42;  DB 4;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 7.9;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 13
US-09-726-653-3
; Sequence 3, Application US/09726653
; Patent No. 6680192
; GENERAL INFORMATION:
;  APPLICANT: LERNER, Richard A.
;  APPLICANT:  WINTER, Gregory P.
;  APPLICANT:  RIECHMAN, Lutz
;  APPLICANT:  HUSE, William D.
;  APPLICANT:  SORGE, Joseph A.
;  TITLE OF INVENTION: A METHOD FOR PRODUCING POLYMERS HAVING A PRESELECTED ACTIVITY
;  FILE REFERENCE: 062710013DVUS01
;  CURRENT APPLICATION NUMBER: US/09/726,653
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 07/941,761
;  PRIOR FILING DATE: 1992-09-04
;  PRIOR APPLICATION NUMBER: 07/799,772
;  PRIOR FILING DATE: 1991-11-27
;  PRIOR APPLICATION NUMBER: 07/496,522
;  PRIOR FILING DATE: 1990-03-20
;  PRIOR APPLICATION NUMBER: 07/410,716
;  PRIOR FILING DATE: 1989-09-20
;  PRIOR APPLICATION NUMBER: 07/352,927
;  PRIOR FILING DATE: 1989-05-16
;  PRIOR APPLICATION NUMBER: 07/411,058
;  PRIOR FILING DATE: 1989-09-21
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(123)
;   OTHER INFORMATION: HPCM1-hybridoma
US-09-726-653-3

  Query Match             82.4%;  Score 42;  DB 4;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 7.9;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 14
US-09-726-653-7
; Sequence 7, Application US/09726653
; Patent No. 6680192
; GENERAL INFORMATION:
;  APPLICANT: LERNER, Richard A.
;  APPLICANT:  WINTER, Gregory P.
;  APPLICANT:  RIECHMAN, Lutz
;  APPLICANT:  HUSE, William D.
;  APPLICANT:  SORGE, Joseph A.
;  TITLE OF INVENTION: A METHOD FOR PRODUCING POLYMERS HAVING A PRESELECTED ACTIVITY
;  FILE REFERENCE: 062710013DVUS01
;  CURRENT APPLICATION NUMBER: US/09/726,653
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 07/941,761
;  PRIOR FILING DATE: 1992-09-04
;  PRIOR APPLICATION NUMBER: 07/799,772
;  PRIOR FILING DATE: 1991-11-27
;  PRIOR APPLICATION NUMBER: 07/496,522
;  PRIOR FILING DATE: 1990-03-20
;  PRIOR APPLICATION NUMBER: 07/410,716
;  PRIOR FILING DATE: 1989-09-20
;  PRIOR APPLICATION NUMBER: 07/352,927
;  PRIOR FILING DATE: 1989-05-16
;  PRIOR APPLICATION NUMBER: 07/411,058
;  PRIOR FILING DATE: 1989-09-21
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;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(123)
;   OTHER INFORMATION: HPCG13-hybridoma
US-09-726-653-7

  Query Match             82.4%;  Score 42;  DB 4;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 7.9;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 15
US-09-726-653-9
; Sequence 9, Application US/09726653
; Patent No. 6680192
; GENERAL INFORMATION:
;  APPLICANT: LERNER, Richard A.
;  APPLICANT:  WINTER, Gregory P.
;  APPLICANT:  RIECHMAN, Lutz
;  APPLICANT:  HUSE, William D.
;  APPLICANT:  SORGE, Joseph A.
;  TITLE OF INVENTION: A METHOD FOR PRODUCING POLYMERS HAVING A PRESELECTED ACTIVITY
;  FILE REFERENCE: 062710013DVUS01
;  CURRENT APPLICATION NUMBER: US/09/726,653
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 07/941,761
;  PRIOR FILING DATE: 1992-09-04
;  PRIOR APPLICATION NUMBER: 07/799,772
;  PRIOR FILING DATE: 1991-11-27
;  PRIOR APPLICATION NUMBER: 07/496,522
;  PRIOR FILING DATE: 1990-03-20
;  PRIOR APPLICATION NUMBER: 07/410,716
;  PRIOR FILING DATE: 1989-09-20
;  PRIOR APPLICATION NUMBER: 07/352,927
;  PRIOR FILING DATE: 1989-05-16
;  PRIOR APPLICATION NUMBER: 07/411,058
;  PRIOR FILING DATE: 1989-09-21
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(123)
;   OTHER INFORMATION: HPCG11-hybridoma
US-09-726-653-9

  Query Match             82.4%;  Score 42;  DB 4;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 7.9;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


Search completed: September 11, 2005, 02:57:37
Job time : 26.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:43:25 ; Search time 100.444 Seconds
(without alignments)
40.785 Million cell updates/sec

Title: US-10-684-957-37
Perfect score: 51
Sequence: 1 GSYWYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	94.1	123	1	HV24_MOUSE	P01793 mus musculu
2	48	94.1	470	2	Q7TMK1	Q7tmk1 mus musculu
3	46	90.2	116	2	Q9UL89	Q9ul89 homo sapien
4	44	86.3	480	2	Q91XE1	Q91xe1 mus musculu
5	42	82.4	122	1	HV21_MOUSE	P01790 mus musculu
6	42	82.4	123	1	HV18_MOUSE	P01787 mus musculu
7	42	82.4	123	1	HV19_MOUSE	P01788 mus musculu
8	42	82.4	144	2	Q924P5	Q924p5 mus musculu
9	42	82.4	357	2	Q8U6E8	Q8u6e8 agrobacteri
10	41	80.4	502	2	Q820T6	Q820t6 enterococcu
11	40	78.4	342	2	Q719E3	Q719e3 vitis ripar
12	40	78.4	388	2	Q6F9F9	Q6f9f9 acinetobact
13	40	78.4	472	2	Q8M8U0	Q8m8u0 vitis vinif
14	40	78.4	523	2	Q89SC8	Q89sc8 bradyrhizob
15	39	76.5	122	1	HV20_MOUSE	P01789 mus musculu
16	39	76.5	165	2	Q8G5I4	Q8g5i4 bifidobacte
17	39	76.5	286	1	HTX1_METAC	Q8thh5 methanosarc
18	39	76.5	286	2	Q728V8	Q728v8 desulfovibr
19	39	76.5	287	1	HTX1_METMA	Q8pxi2 methanosarc
20	39	76.5	314	2	Q7RW71	Q7rw71 neurospora
21	39	76.5	316	2	Q667C2	Q667c2 yersinia ps
22	39	76.5	316	2	Q8ZHR3	Q8zhr3 yersinia pe
23	39	76.5	364	2	Q8KKU1	Q8kku1 rhizobium e
24	39	76.5	364	2	Q8UK25	Q8uk25 agrobacteri
25	39	76.5	475	2	Q6MZQ6	Q6mzq6 homo sapien
26	39	76.5	655	2	Q62BC6	Q62bc6 burkholderi
27	39	76.5	655	2	Q63MC5	Q63mc5 burkholderi
28	39	76.5	891	2	Q7XM05	Q7xm05 oryza sativ
29	38	74.5	108	2	Q6H0Z5	Q6h0z5 sulfolobus
30	38	74.5	117	1	HV13_MOUSE	P01757 mus musculu
31	38	74.5	123	1	HV23_MOUSE	P01792 mus musculu
32	38	74.5	209	2	Q6WU92	Q6wu92 lactobacill
33	38	74.5	347	1	C5AR_MOUSE	P30993 mus musculu
34	38	74.5	360	2	Q74GQ2	Q74gq2 geobacter s
35	38	74.5	360	2	Q82X92	Q82x92 nitrosomona
36	38	74.5	676	2	Q9YE45	Q9ye45 aeropyrum p
37	38	74.5	768	2	Q97J01	Q97j01 clostridium
38	38	74.5	802	2	Q7VMP1	Q7vmp1 haemophilus
39	38	74.5	3198	2	Q9U8G8	Q9u8g8 manduca sex
40	37	72.5	29	2	Q6I9I1	Q6i9i1 mus musculu
41	37	72.5	117	2	Q6IVE4	Q6ive4 strongyloce
42	37	72.5	157	1	BRIX_METAC	Q8tq11 methanosarc
43	37	72.5	222	2	O90303	O90303 rice tungro
44	37	72.5	225	2	O08377	O08377 mycobacteri
45	37	72.5	225	2	Q7VEZ1	Q7vez1 mycobacteri

ALIGNMENTS

RESULT 1
HV24_MOUSE
ID HV24_MOUSE STANDARD; PRT; 123 AA.
AC P01793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V region HPCG13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
RT IgM counterparts.";
RL Nature 291:29-34(1981).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; F93256; AVMS13.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 114 Ig-like.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13808 MW; 6599F256ECCEDE50 CRC64;

Query Match 94.1%; Score 48; DB 1; Length 123;
Best Local Similarity 87.5%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GSYWYFDL 8
              |||||||:
Db        105 GSYWYFDV 112
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RESULT 2
Q7TMK1
ID Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein AI324046.
GN Name=AI324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
DR   HSSP; P01865; 1KB5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match             94.1%;  Score 48;  DB 2;  Length 470;
  Best Local Similarity   87.5%;  Pred. No. 10;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |||||||:
Db        122 GSYWYFDV 129


RESULT 3
Q9UL89
ID   Q9UL89      PRELIMINARY;      PRT;   116 AA.
AC   Q9UL89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035025; AAD56261.1; -.
DR   PIR; PH0870; PH0870.
DR   PIR; PH1671; PH1671.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12605 MW;  C8F9131DE13EA898 CRC64;

  Query Match             90.2%;  Score 46;  DB 2;  Length 116;
  Best Local Similarity   87.5%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | ||||||
Db         98 GPYWYFDL 105


RESULT 4
Q91XE1
ID   Q91XE1      PRELIMINARY;      PRT;   480 AA.
AC   Q91XE1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein (Fragment).
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010798; AAH10798.1; -.
DR   HSSP; P01789; 1MCP.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT   NON_TER       1      1
SQ   SEQUENCE   480 AA;  51936 MW;  20B9234EEF2B41ED CRC64;
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  Query Match             86.3%;  Score 44;  DB 2;  Length 480;
  Best Local Similarity   75.0%;  Pred. No. 47;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db        117 GDYWYFDV 124


RESULT 5
HV21_MOUSE
ID   HV21_MOUSE     STANDARD;      PRT;   122 AA.
AC   P01790;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V region M511.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81054880; PubMed=6776528;
RA   Robinson E.A., Appella E.;
RT   "Complete amino acid sequence of a mouse immunoglobulin alpha chain
RT   (MOPC 511).";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC       binds phosphorylcholine.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1    114       Ig-like.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13652 MW;  9F4837731EA50207 CRC64;

  Query Match             82.4%;  Score 42;  DB 1;  Length 122;
  Best Local Similarity   85.7%;  Pred. No. 27;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        105 SYWYFDV 111


RESULT 6
HV18_MOUSE
ID   HV18_MOUSE     STANDARD;      PRT;   123 AA.
AC   P01787;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE (TEPC 15).
RX   MEDLINE=76222762; PubMed=819932;
RA   Rudikoff S., Potter M.;
RT   "Size differences among immunoglobulin heavy chains from
RT   phosphorylcholine-binding proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN   [2]
RP   SEQUENCE FROM N.A. (H107).
RX   MEDLINE=80199926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
RA   Early P., Huang H., Davis M., Calame K., Hood L.;
RT   "An immunoglobulin heavy chain variable region gene is generated from
RT   three segments of DNA: VH, D and JH.";
RL   Cell 19:981-992(1980).
RN   [3]
RP   SEQUENCE (S107).
RX   MEDLINE=76110488; PubMed=813561;
RX   DOI=10.1146/annurev.ge.09.120175.001513;
RA   Rudikoff S., Barstad P., Potter M., Hood L.;
RL   Unpublished results, cited by:
RL   Hood L., Campbell J.H., Elgin S.C.R.;
RL   Annu. Rev. Genet. 9:305-353(1975).
RN   [4]
RP   SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX   MEDLINE=81197602; PubMed=7231520;
RA   Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT   "IgG antibodies to phosphorylcholine exhibit more diversity than their
RT   IgM counterparts.";
RL   Nature 291:29-34(1981).
CC   -!- MISCELLANEOUS: All those sequence appears to be identical.
CC   -!- MISCELLANEOUS: These chains were isolated from myeloma and
CC       hybridoma proteins that bind phosphorylcholine.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A93804; AVMST5.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1    114       Ig-like.
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  13777 MW;  9D58086DE12F7000 CRC64;

  Query Match             82.4%;  Score 42;  DB 1;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 27;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 7
HV19_MOUSE
ID   HV19_MOUSE     STANDARD;      PRT;   123 AA.
AC   P01788;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V region H8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RA   Barstad P.;
RL   Thesis (1975), California Institute of Technology / Pasadena, U.S.A.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC       binds phosphorylcholine.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1    114       Ig-like.
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  13805 MW;  9D581401912F7000 CRC64;
```

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  Query Match             82.4%;  Score 42;  DB 1;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 27;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 8
Q924P5
ID   Q924P5      PRELIMINARY;      PRT;   144 AA.
AC   Q924P5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069920; BAB63936.1; -.
DR   PIR; PH1137; PH1137.
DR   PIR; S26744; S26744.
DR   HSSP; P01751; 1A6W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  15865 MW;  CD07BE97E95C1B27 CRC64;

  Query Match             82.4%;  Score 42;  DB 2;  Length 144;
  Best Local Similarity   85.7%;  Pred. No. 31;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        102 SYWYFDV 108


RESULT 9
Q8U6E8
ID   Q8U6E8      PRELIMINARY;      PRT;   357 AA.
AC   Q8U6E8; Q7CW22;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein Atu4859 (AGR_L_56p).
GN   OrderedLocusNames=AGR_L_56, Atu4859;
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dupont;
RX   MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Cereon;
RX   MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
DR   EMBL; AE009415; AAL45653.1; -.
DR   EMBL; AE008199; AAK88588.1; -.
DR   PIR; AG3154; AG3154.
DR   PIR; B98133; B98133.
DR   InterPro; IPR009213; UCP031854.
DR   PIRSF; PIRSF031854; UCP031854; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   357 AA;  39468 MW;  E1BED6637E4509A6 CRC64;

  Query Match             82.4%;  Score 42;  DB 2;  Length 357;
  Best Local Similarity   85.7%;  Pred. No. 74;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              :||||||
Db         43 NYWYFDL 49


RESULT 10
Q820T6
ID   Q820T6      PRELIMINARY;      PRT;   502 AA.
AC   Q820T6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   FtsK/SpoIIIE family protein.
GN   OrderedLocusNames=EF2533;
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX   NCBI_TaxID=1351;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=V583 / ATCC 700802;
RX   MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA   Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA   Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA   Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA   Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA   Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA   Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA   Fraser C.M.;
RT   "Role of mobile DNA in the evolution of vancomycin-resistant
RT   Enterococcus faecalis.";
RL   Science 299:2071-2074(2003).
DR   EMBL; AE016955; AAO82246.1; -.
DR   TIGR; EF2533; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR002543; FtsK_SpoIIIE.
DR   InterPro; IPR008262; Lipase_AS.
DR   Pfam; PF01580; FtsK_SpoIIIE; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS50901; FTSK; 1.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW   ATP-binding; Complete proteome.
```

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SQ   SEQUENCE   502 AA;  57509 MW;  4CDB8892AAF3FCB5 CRC64;

  Query Match             80.4%;  Score 41;  DB 2;  Length 502;
  Best Local Similarity   85.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFD 7
              | |||||
Db        210 GLYWYFD 216


RESULT 11
Q719E3
ID   Q719E3      PRELIMINARY;      PRT;   342 AA.
AC   Q719E3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Maturase K (Fragment).
GN   Name=matK;
OS   Vitis riparia (Frost grape) (Vitis vulpina).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   Vitaceae; Vitis.
OX   NCBI_TaxID=96939;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hilu K.W., Borsch T., Mueller K., Soltis D.E., Soltis P.S.,
RA   Savolainen V., Chase M., Powell M., Alice L.A., Evans R., Sanquet H.,
RA   Neinhuis C., Slotta T.A.B., Rohwer J.G., Campbell C.S., Catrou L.W.;
RT   "Angiosperm phlyogeny based on matK sequence information.";
RL   Am. J. Bot. 90:1758-1776(2003).
DR   EMBL; AF542593; AAQ11455.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0008380; P:RNA splicing; IEA.
DR   InterPro; IPR008998; Agglutinin.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR002866; MatK_N.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF01824; MatK_N; 1.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER     342    342
SQ   SEQUENCE   342 AA;  40595 MW;  01D14C5FCE1CF888 CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 342;
  Best Local Similarity   62.5%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | :||||:
Db        326 GRFWYFDI 333


RESULT 12
Q6F9F9
ID   Q6F9F9      PRELIMINARY;      PRT;   388 AA.
AC   Q6F9F9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=ACIAD2540;
OS   Acinetobacter sp. (strain ADP1).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Moraxellaceae; Acinetobacter.
OX   NCBI_TaxID=62977;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA   Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA   Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT   "Unique features revealed by the genome sequence of Acinetobacter sp.
RT   ADP1, a versatile and naturally transformation competent bacterium.";
RL   Nucleic Acids Res. 0:0-0(2004).
DR   EMBL; CR543861; CAG69305.1; -.
KW   Complete proteome.
SQ   SEQUENCE   388 AA;  43284 MW;  F4C1CEB775AFEF56 CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 388;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |||||  |:
Db        223 GSYWYSDV 230


RESULT 13
Q8M8U0
ID   Q8M8U0      PRELIMINARY;      PRT;   472 AA.
AC   Q8M8U0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Maturase (Fragment).
GN   Name=matK;
OS   Vitis vinifera (Grape).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   Vitaceae; Vitis.
OX   NCBI_TaxID=29760;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bremer B., Bremer K., Heidari N., Erixon P., Olmstead R.G.,
RA   Anderberg A.A., Kallersjo M., Barkhordarian E.;
RT   "Phylogenetics of asterids based on 3 coding and 3 non-coding
RT   chloroplast DNA markers and the utility of non-coding DNA at higher
RT   taxonomic levels.";
RL   Mol. Phylogenet. Evol. 24:273-300(2002).
DR   EMBL; AJ429274; CAD22170.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0008380; P:RNA splicing; IEA.
DR   InterPro; IPR008998; Agglutinin.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR002866; MatK_N.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF01824; MatK_N; 1.
KW   Chloroplast.
FT   NON_TER       1      1
SQ   SEQUENCE   472 AA;  55654 MW;  A5A1E7EE65E962B3 CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 472;
  Best Local Similarity   62.5%;  Pred. No. 2e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | :||||:
Db        455 GRFWYFDI 462


RESULT 14
Q89SC8
ID   Q89SC8      PRELIMINARY;      PRT;   523 AA.
AC   Q89SC8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Blr2472 protein.
GN   OrderedLocusNames=blr2472;
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA110;
RX   MEDLINE=22484998; PubMed=12597275;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
DR   EMBL; AP005943; BAC47737.1; -.
KW   Complete proteome.
SQ   SEQUENCE   523 AA;  57529 MW;  8F9EC488EFF67490 CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 523;
  Best Local Similarity   71.4%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFD 7
              |::||||
Db        248 GTFWYFD 254


RESULT 15
HV20_MOUSE
ID   HV20_MOUSE     STANDARD;      PRT;   122 AA.
AC   P01789;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region M603.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80199926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
RA   Early P., Huang H., Davis M., Calame K., Hood L.;
RT   "An immunoglobulin heavy chain variable region gene is generated from
RT   three segments of DNA: VH, D and JH.";
RL   Cell 19:981-992(1980).
RN   [2]
RP   SEQUENCE OF 1-120.
RX   MEDLINE=75017346; PubMed=4213527;
RA   Rudikoff S., Potter M.;
RT   "Variable region sequence of the heavy chain from a phosphorylcholine
RT   binding myeloma protein.";
RL   Biochemistry 13:4033-4038(1974).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
RX   MEDLINE=75065510; PubMed=4530984;
RA   Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
RA   Davies D.R.;
RT   "The three-dimensional structure of a phosphorylcholine-binding mouse
RT   immunoglobulin Fab and the nature of the antigen binding site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC       binds phosphorylcholine.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; B90795; AVMS63.
DR   PDB; 1MCP; X-ray; H=1-122.
DR   PDB; 2MCP; X-ray; H=1-122.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1    121       Ig-like.
FT   SITE         33     33       H-bond with the phosphate group of
FT                                 phosphorylcholine.
FT   SITE         52     52       H-bond with the phosphate group of
FT                                 phosphorylcholine.
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       17     25
FT   TURN         30     31
FT   STRAND       33     39
FT   TURN         41     42
FT   STRAND       46     50
FT   TURN         54     55
FT   STRAND       61     61
FT   TURN         64     69
FT   STRAND       70     75
FT   TURN         76     79
FT   STRAND       80     86
FT   HELIX        90     92
FT   STRAND       94    103
FT   STRAND      107    112
FT   STRAND      116    120
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13626 MW;  BA2C864438B64F0F CRC64;

  Query Match             76.5%;  Score 39;  DB 1;  Length 122;
  Best Local Similarity   75.0%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              || ||||:
Db        104 GSTWYFDV 111


Search completed: September 11, 2005, 02:55:40
Job time : 103.444 secs
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:44:10 ; Search time 20.8889 Seconds
(without alignments)
36.849 Million cell updates/sec

Title: US-10-684-957-37
Perfect score: 51
Sequence: 1 GSYWYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	94.1	111	2	S26463	Ig heavy chain V r
2	48	94.1	122	2	B30515	Ig heavy chain V r
3	48	94.1	123	1	AVMS13	Ig heavy chain V r
4	45	88.2	112	2	S26327	Ig heavy chain V r
5	45	88.2	115	2	S13694	Ig heavy chain V r
6	45	88.2	116	2	S13691	Ig heavy chain V r
7	45	88.2	137	2	S03326	Ig heavy chain pre
8	44	86.3	91	2	S13689	Ig heavy chain V r
9	43	84.3	111	2	S13693	Ig heavy chain V r
10	42	82.4	101	2	S13692	Ig heavy chain V r
11	42	82.4	107	2	PH0987	Ig heavy chain V r
12	42	82.4	112	2	PH1022	Ig heavy chain V r
13	42	82.4	123	1	AVMST5	Ig heavy chain VH1
14	42	82.4	123	2	PL0017	Ig heavy chain V-D
15	42	82.4	123	2	B30556	Ig heavy chain V r
16	42	82.4	123	2	D30539	Ig heavy chain V r
17	42	82.4	123	2	A30540	Ig heavy chain V r
18	42	82.4	124	1	AVMS51	Ig heavy chain V r
19	42	82.4	357	2	B98133	hypothetical prote
20	42	82.4	357	2	AG3154	conserved hypothet
21	41	80.4	113	2	PH1663	Ig heavy chain V r
22	41	80.4	121	2	S31104	Ig heavy chain (su
23	41	80.4	138	2	S31666	Ig heavy chain V r
24	40	78.4	107	2	PH1013	Ig heavy chain V r
25	40	78.4	108	2	PH1656	Ig heavy chain V r
26	39	76.5	106	2	PH1002	Ig heavy chain V r
27	39	76.5	112	2	S13690	Ig heavy chain V r
28	39	76.5	121	2	D30556	Ig heavy chain V r
29	39	76.5	122	1	AVMS63	Ig heavy chain V r
30	39	76.5	123	2	PT0354	Ig heavy chain V r
31	39	76.5	316	2	AD0101	probable exported
32	39	76.5	364	2	AE3196	conserved hypothet
33	38	74.5	17	2	S26744	Ig heavy chain J r
34	38	74.5	31	2	B49038	Ig lambda chain V
35	38	74.5	38	2	C49038	Ig lambda chain V
36	38	74.5	56	2	E49038	Ig lambda chain V
37	38	74.5	58	2	D49038	Ig lambda chain V
38	38	74.5	91	2	PH1004	Ig heavy chain V r
39	38	74.5	108	2	PH1006	Ig heavy chain V r
40	38	74.5	110	2	S13688	Ig heavy chain V r
41	38	74.5	111	2	S13687	Ig heavy chain V r
42	38	74.5	112	2	S13686	Ig heavy chain V r
43	38	74.5	112	2	S13685	Ig heavy chain V r
44	38	74.5	113	2	PH1018	Ig heavy chain V r
45	38	74.5	114	2	S36280	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S26463
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26463
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <KAV>
A;Cross-references: EMBL:X59113; NID:g51922; PIDN:CAA41839.1; PID:g51923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 94.1%; Score 48; DB 2; Length 111;
Best Local Similarity 87.5%; Pred. No. 0.49;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
|||||||:
Db 94 GSYWYFDV 101

RESULT 2
B30515
Ig heavy chain V region (5-1E4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 16-Aug-1996
C;Accession: B30515
R;Feeney, A.J.; Clarke, S.H.; Mosier, D.E.
J. Immunol. 141, 1267-1272, 1988
A;Title: Specific H chain junctional diversity may be required for non-T15 antibodies t
A;Reference number: A30515; MUID:88285740; PMID:3135325
A;Accession: B30515
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <FEE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>

Query Match 94.1%; Score 48; DB 2; Length 122;
Best Local Similarity 87.5%; Pred. No. 0.53;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
|||||||:
Db 104 GSYWYFDV 111

```
RESULT 3
AVMS13
Ig heavy chain V region (HPCG13) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: F93256
R;Gearhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.
Nature 291, 29-34, 1981
A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count
A;Reference number: A93256; MUID:81197602; PMID:7231520
A;Accession: F93256
A;Molecule type: protein
A;Residues: 1-123 <GEA>
A;Cross-references: UNIPROT:P01793
A;Note: the possibility that some of the diversity seen in sequences of phosphorylcholin
C;Comment: This hybridoma protein binds phosphorylcholine.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

  Query Match             94.1%;  Score 48;  DB 1;  Length 123;
  Best Local Similarity   87.5%;  Pred. No. 0.53;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |||||||:
Db        105 GSYWYFDV 112


RESULT 4
S26327
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26327
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26327
A;Molecule type: mRNA
A;Residues: 1-112 <STA>
A;Cross-references: EMBL:X59192
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-91/Domain: immunoglobulin homology <IMM>

  Query Match             88.2%;  Score 45;  DB 2;  Length 112;
  Best Local Similarity   75.0%;  Pred. No. 1.5;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |:|||||:
Db         94 GNYWYFDV 101


RESULT 5
S13694
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13694
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13694
A;Molecule type: mRNA
A;Residues: 1-115 <PEN>
A;Cross-references: EMBL:X53347; NID:g55240; PIDN:CAA37433.1; PID:g930210
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.2%;  Score 45;  DB 2;  Length 115;
  Best Local Similarity   75.0%;  Pred. No. 1.5;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |:|||||:
Db        100 GNYWYFDV 107


RESULT 6
S13691
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13691
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13691
A;Molecule type: mRNA
A;Residues: 1-116 <PEN>
A;Cross-references: EMBL:X53344; NID:g55235; PIDN:CAA37430.1; PID:g930207
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.2%;  Score 45;  DB 2;  Length 116;
  Best Local Similarity   75.0%;  Pred. No. 1.5;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |:|||||:
Db        100 GNYWYFDV 107


RESULT 7
S03326
Ig heavy chain precursor V-D-J region (clone pCP12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: S03326
R;Reininger, L.; Kaushik, A.; Izui, S.; Jaton, J.C.
Eur. J. Immunol. 18, 1521-1526, 1988
A;Title: A member of a new V(H) gene family encodes antibromelinized mouse red blood cel
A;Reference number: S03326; MUID:89052754; PMID:2903828
A;Accession: S03326
A;Molecule type: mRNA
A;Residues: 1-137 <REI>
A;Cross-references: EMBL:Y00743; NID:g52483; PIDN:CAA68712.1; PID:g52484
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region pCP12 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-120/Domain: D region #status predicted <DRE>
F;121-137/Domain: J region #status predicted <JRE>

  Query Match             88.2%;  Score 45;  DB 2;  Length 137;
  Best Local Similarity   75.0%;  Pred. No. 1.8;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              |:|||||:
Db        119 GNYWYFDV 126


RESULT 8
S13689
```

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Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
C;Accession: S13689
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13689
A;Molecule type: mRNA
A;Residues: 1-91 <PEN>
A;Cross-references: EMBL:X53342
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             86.3%;  Score 44;  DB 2;  Length 91;
  Best Local Similarity   75.0%;  Pred. No. 1.8;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db         80 GGYWYFDV 87


RESULT 9
S13693
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S13693
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13693
A;Molecule type: mRNA
A;Residues: 1-111 <PEN>
A;Cross-references: EMBL:X53346
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.3%;  Score 43;  DB 2;  Length 111;
  Best Local Similarity   75.0%;  Pred. No. 3.1;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db        100 GPYWYFDV 107


RESULT 10
S13692
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
C;Accession: S13692
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13692
A;Molecule type: mRNA
A;Residues: 1-101 <PEN>
A;Cross-references: EMBL:X53345
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             82.4%;  Score 42;  DB 2;  Length 101;
  Best Local Similarity   85.7%;  Pred. No. 4.1;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db         84 SYWYFDV 90


RESULT 11
PH0987
Ig heavy chain V region (clone 163.47) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0987
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0987
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.4%;  Score 42;  DB 2;  Length 107;
  Best Local Similarity   75.0%;  Pred. No. 4.4;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              | |||||:
Db         99 GIYWYFDV 106


RESULT 12
PH1022
Ig heavy chain V region (clone 202.17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1022
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1022
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-112 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

  Query Match             82.4%;  Score 42;  DB 2;  Length 112;
  Best Local Similarity   85.7%;  Pred. No. 4.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        105 SYWYFDV 111


RESULT 13
AVMST5
Ig heavy chain VH1 regions (TEPC 15, S107, H8, HPCM1, HPCM2, HPCM3, 224.2B8, 224.2G3, 25
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A93804; A90795; A94474; A94449; A93256; C30539; I30539; B30539; A02070; A90
R;Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 73, 2109-2112, 1976
A;Title: Size differences among immunoglobulin heavy chains from phosphorylcholine-bindi
A;Reference number: A93804; MUID:76222762; PMID:819932
A;Contents: TEPC 15
A;Accession: A93804
A;Molecule type: protein
```

```
A;Residues: 1-123 <RUD>
A;Cross-references: UNIPROT:P01787
R;Early, P.; Huang, H.; Davis, M.; Calame, K.; Hood, L.
Cell 19, 981-992, 1980
A;Title: An immunoglobulin heavy chain variable region gene is generated from three segm
A;Reference number: A90795; MUID:80199926; PMID:6769593
A;Contents: S107
A;Accession: A90795
A;Molecule type: DNA
A;Residues: 1-101 <EAR>
A;Note: sequence determined from the germline H107 gene
R;Rudikoff, S.; Barstad, P.; Potter, M.; Hood, L.
unpublished results, cited by Hood, L., Campbell, J.H., and Elgin, S.C.R., Annu. Rev. Ge
A;Reference number: A94474
A;Contents: S107
A;Accession: A94474
A;Molecule type: protein
A;Residues: 1-123 <RU2>
R;Barstad, P.
Ph.D. thesis, California Institute of Technology, Pasadena, 1975, cited by Hood, L., Cam
A;Reference number: A94449
A;Contents: H8
A;Accession: A94449
A;Molecule type: protein
A;Residues: 1-104,'B',106-123 <BAR>
R;Gearhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.
Nature 291, 29-34, 1981
A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count
A;Reference number: A93256; MUID:81197602; PMID:7231520
A;Accession: A93256
A;Molecule type: protein
A;Residues: 1-123 <GEA>
A;Experimental source: hybridoma proteins HPCM1, HPCM2, HPCM3
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: C30539
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-123 <CLA>
A;Experimental source: hybridoma proteins 224.2B8, 224.2G3
A;Accession: I30539
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-123 <CL2>
A;Experimental source: hybridoma proteins 252.5E11, 253.12G5
A;Accession: B30539
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-121 <CL3>
A;Experimental source: hybridoma protein 174.2E11
C;Comment: These chains were isolated from myeloma and hybridoma proteins that bind phos
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

  Query Match             82.4%;  Score 42;  DB 1;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 5;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 14
PL0017
Ig heavy chain V-D-J region (P28) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C;Accession: PL0017
R;Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A;Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor
A;Reference number: JL0029; MUID:88171315; PMID:3127529
A;Accession: PL0017
A;Molecule type: mRNA
A;Residues: 1-123 <CHI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-101/Domain: V region (fragment) <VRE>
F;15-100/Domain: immunoglobulin homology <IMM>
F;102-106/Domain: D region <DRE>
F;107-123/Domain: J region (fragment) <JRE>

  Query Match             82.4%;  Score 42;  DB 2;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 5;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


RESULT 15
B30556
Ig heavy chain V region (2B2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
C;Accession: B30556
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A;Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced wit
A;Reference number: A30556; MUID:87196439; PMID:3106498
A;Accession: B30556
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <CLA>
A;Note: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

  Query Match             82.4%;  Score 42;  DB 2;  Length 123;
  Best Local Similarity   85.7%;  Pred. No. 5;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYWYFDL 8
              ||||||:
Db        106 SYWYFDV 112


Search completed: September 11, 2005, 02:56:32
Job time : 21.8889 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 02:40:25 ; Search time 105.333 Seconds
(without alignments)
29.374 Million cell updates/sec

Title: US-10-684-957-37
Perfect score: 51
Sequence: 1 GSYWYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	8	8	ADS87944	Ads87944 Anti-IFN-
2	51	100.0	8	8	ADS94941	Ads94941 Anti-IFN-
3	51	100.0	117	8	ADS87917	Ads87917 Anti-IFN-
4	51	100.0	117	8	ADS87921	Ads87921 Anti-IFN-
5	51	100.0	117	8	ADS87937	Ads87937 Anti-IFN-
6	51	100.0	117	8	ADS94914	Ads94914 Anti-IFN-
7	51	100.0	117	8	ADS94934	Ads94934 Anti-IFN-
8	51	100.0	117	8	ADS94918	Ads94918 Anti-IFN-
9	51	100.0	447	8	ADS87928	Ads87928 Anti-IFN-
10	51	100.0	447	8	ADS87926	Ads87926 Anti-IFN-
11	51	100.0	447	8	ADS87939	Ads87939 Anti-IFN-
12	51	100.0	447	8	ADS94936	Ads94936 Anti-IFN-
13	51	100.0	447	8	ADS94923	Ads94923 Anti-IFN-
14	51	100.0	447	8	ADS94925	Ads94925 Anti-IFN-
15	45	88.2	10	7	ADD69225	Add69225 Human hea
16	45	88.2	10	7	ADD69228	Add69228 Human hea
17	45	88.2	15	8	ADG31813	Adg31813 Experimen
18	45	88.2	19	8	ADG31815	Adg31815 Anti-VEGF
19	45	88.2	19	8	ADG31817	Adg31817 Anti-VEGF
20	45	88.2	19	8	ADG31825	Adg31825 Variant p
21	45	88.2	19	8	ADG31820	Adg31820 Anti-VEGF
22	45	88.2	19	8	ADG31816	Adg31816 Anti-VEGF
23	45	88.2	19	8	ADG31823	Adg31823 Anti-VEGF
24	45	88.2	19	8	ADG31824	Adg31824 Anti-VEGF
25	45	88.2	20	5	ABP47138	Abp47138 Human BLy
26	45	88.2	20	7	ADG97965	Adg97965 scFV VHCD
27	45	88.2	26	8	ADG31857	Adg31857 Anti-VEGF
28	45	88.2	26	8	ADG31840	Adg31840 Anti-VEGF
29	45	88.2	26	8	ADG31843	Adg31843 Anti-VEGF
30	45	88.2	26	8	ADG31842	Adg31842 Anti-VEGF
31	45	88.2	26	8	ADG31853	Adg31853 Anti-VEGF
32	45	88.2	26	8	ADG31852	Adg31852 Anti-VEGF
33	45	88.2	26	8	ADG31891	Adg31891 Anti-VEGF
34	45	88.2	113	7	ADD69210	Add69210 Human ant
35	45	88.2	117	8	ADP22112	Adp22112 Human ant
36	45	88.2	119	7	ADD69209	Add69209 Human ant
37	45	88.2	119	8	ADO44272	Ado44272 Primer in
38	45	88.2	120	8	ADO44280	Ado44280 Humanised
39	45	88.2	120	8	ADO44274	Ado44274 Consensus
40	45	88.2	120	8	ADO44271	Ado44271 Sequence
41	45	88.2	256	5	ABP46108	Abp46108 Human BLy
42	45	88.2	256	7	ADG96935	Adg96935 Single ch
43	43	84.3	17	3	AAB06394	Aab06394 Randomise
44	43	84.3	17	3	AAB06392	Aab06392 Randomise
45	43	84.3	17	3	AAB06391	Aab06391 Randomise

ALIGNMENTS

RESULT 1
ADS87944
ID ADS87944 standard; peptide; 8 AA.
XX
AC ADS87944;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR3 SEQ ID NO:37.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87953.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 1; SEQ ID NO 37; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising

```
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC   (CDR), which is used in the exemplification of the present invention.
XX
SQ   Sequence 8 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db          1 GSYWYFDL 8


RESULT 2
ADS94941
ID   ADS94941 standard; peptide; 8 AA.
XX
AC   ADS94941;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody heavy chain CDR3 SEQ ID NO:37.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
DR   N-PSDB; ADS94950.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 1; SEQ ID NO 37; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC   (CDR), which is used in the exemplification of the present invention.
XX
SQ   Sequence 8 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYWYFDL 8
              ||||||||
Db          1 GSYWYFDL 8


RESULT 3
ADS87917
ID   ADS87917 standard; protein; 117 AA.
XX
AC   ADS87917;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:10.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
DR   N-PSDB; ADS87916.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
```

PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 10; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 4
ADS87921
ID ADS87921 standard; protein; 117 AA.
XX
AC ADS87921;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:14.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87920.
XX

PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 5
ADS87937
ID ADS87937 standard; protein; 117 AA.
XX
AC ADS87937;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:30.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX

DR WPI; 2004-348323/32.
DR N-PSDB; ADS87963.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 30; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 6
ADS94914
ID ADS94914 standard; protein; 117 AA.
XX
AC ADS94914;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:10.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94913.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 10; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 7
ADS94934
ID ADS94934 standard; protein; 117 AA.
XX
AC ADS94934;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:30.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX

PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94960.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 30; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 8
ADS94918
ID ADS94918 standard; protein; 117 AA.
XX
AC ADS94918;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:14.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94917.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 9
ADS87928
ID ADS87928 standard; protein; 447 AA.
XX
AC ADS87928;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX

OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 21; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 51; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 10
ADS87926
ID ADS87926 standard; protein; 447 AA.
XX
AC ADS87926;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 19; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 51; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 11
ADS87939
ID ADS87939 standard; protein; 447 AA.
XX
AC ADS87939;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;

KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 32; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 51; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 12
ADS94936
ID ADS94936 standard; protein; 447 AA.
XX
AC ADS94936;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 32; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 51; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 13
ADS94923
ID ADS94923 standard; protein; 447 AA.
XX
AC ADS94923;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;

KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 19; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 51; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 14
ADS94925
ID ADS94925 standard; protein; 447 AA.
XX
AC ADS94925;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 21; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 51; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYWYFDL 8
||||||||
Db 99 GSYWYFDL 106

RESULT 15
ADD69225
ID ADD69225 standard; peptide; 10 AA.
XX
AC ADD69225;

XX
DT 15-JAN-2004 (first entry)
XX
DE Human heavy chain variable region CDR3 peptide - SEQ ID 29.
XX
KW monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 1; SEQ ID NO 29; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as duing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR3 peptide of the invention.
XX
SQ Sequence 10 AA;

Query Match 88.2%; Score 45; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SYWYFDL 8
|||||||
Db 4 SYWYFDL 10

Search completed: September 11, 2005, 02:51:47
Job time : 106.333 secs

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